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159 ISIVSSFALFALLTIAT-----LYCCRRRKEWKNKKRESTAVTLTTLPSELLLDRLHP 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           38 KENYDKYS---EPR----GYPKGERSLNFEELKDWGP---KNVIKMSTPAVNKMPHS-FA 86
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 21.43
Matches 43; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 87 camerrary: Cambridge
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                                                               USA
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67.5
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(without alignments)
205.960 Million cell updates/sec
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1018
1 MEIISSKLFILLTLATSSLL.......KQSRRLLFKKIDDAELKQEK 196
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Sequence 7
Sequence 3
Sequence 2
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
           GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-134-001C-3155
US-09-420-211-2
US-08-257-073-9
PCT-US94-00198-3
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US - 08 - 644 - 271 - 29
US - 09 - 077 - 955 - 33
US - 09 - 077 - 955 - 33
US - 09 - 749 - 588 - 2
US - 09 - 249 - 669 - 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                  using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Match Length
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Sequence 2, Appli
Sequence 2, Appli
Sequence 5, Appli
Sequence 3518, Ap
Sequence 10, Appl
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32, Ap
4378,
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Sequence 6
Sequence 3
Sequence 2
Sequence 2
Sequence 2
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Sequence
Sequence
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                                                                                                                                                                                                                                                                                                                                                              General Information PC/TUS9508493
GENERAL INFORMATION:
APPLICANT: Wood, Clive
APPLICANT: Grauso, Anthony
TITLE OF INVENTION: Novel mlk Receptor Tyrosine Kinases
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: LEGAL AFFAIRS
STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: LAWRY WISK
COMPUTER: COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UMBER: PCT/US95/08493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7.5%; Score 76.5; DB 5;
21.4%; Pred. No. 1.7;
                                                                                                                                                                                                                                    US-09-134-001C-3518
US-08-220-151-10
             09-134-001C-4378
                                                                                 US-09-205-681-3
US-09-045-201A-2
US-09-045-201A-2
US-09-903-800A-6
US-09-213-053-4
US-08-891-640-3
US-08-898-978-2
                                         US-09-299-041-4
US-09-299-041-6
US-08-978-182-3
                                                                                                                                                                                                       US-09-372-858-2
US-08-701-154A-5
                                                                                                                                                                                                                                                                                             ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: G15234A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 496-8824
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Brown, Scott A
REGISTRATION NUMBER: 32,724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
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 793
878
8332
332
332
539
539
7052
11394
11041
11041
11041
301
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MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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63;

63;

32; Mismatches

-- DELVMSNLHS 37

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550 NPWYQRMPLLLINPKLLSLEYPRN----NIEYVRDIGEGAFGRVFQARAPGL--LPYEPFT 603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : |:|| || |||:||
497 ISIVSSPALFALLTIAT-----LYCCRRRKEWKNKKRESTAVTLTLPSELLLDRLHP 549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    87 NIPLRFGRNVQEERSAGATANLPLRSGRNMEVSLVRRV--PNLPQRFGRTTTAKSVCRML 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   604 MVAVKM---LKEBASADMQADF-----QREAALMAEFDNPNIVKLLGVCAVGKPMCLLF 654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      38 KENYDKYS---EPR----GYPKGERSLNFEELKDWGP---KNVIKMSTPAVNKMPHS-FA 86
                APPLICANT: Wood, Clive
APPLICANT: Caruso, Anthony
TITLE OF INVENTION: Novel mlk Receptor Tyrosine Kinases
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 16, Application US/08374834
Patent No. 5656473
GENERAL INPERMATION:
APPLICANT: Valenzuela, et al.
TITLE OF INVENTON:
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/08493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSE: Regeneron Pharmaceuticals, Inc. STREET: 77 old Saw Mill River Road CITY: Tarrytown STATE: New York COUNTRY: USA ZIP: 10591
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 7.5%; Score 76.5; D
Best Local Similarity 21.4%; Pred. No. 3.5;
Matches 43; Conservative 32; Mismatches
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                                                                                                                   ADDRESSEE: LEGAL AFFAIRS
STREET: 87 CambridgePark Drive
CITY: Cambridge
                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A
REGISTRATION NUMBER: 32,724
REFERENCE/DOCKET NUMBER: G152
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 145 SDLCQGSMHSPCANDLFYSMT 165
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (617) 498-824
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 21:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 868 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
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  GENERAL INFORMATION:
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87 NLPLRFGRNVQEERSAGATANLPLRSGRNMEVSLVRRV--PNLPQRFGRTTTAKSVCRML 144
                         266 MVAVKM---LKEEASADMQADF-----OREAALMAEFDNPNIVKLLGVCAVGKPMCLLF 316
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489 ISIVSSFALFALLTIAT-----LYCCRRKEWKNKRESTAVTLTLPSELLLDRLHP 541
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                                                                                                                                                                                                          Sequence 19, Application PC/TUS9508493
GENERAL INFORMATION:
APPLICANT: Wood, Clive
APPLICANT: Garuso, Anthony
TITLE OF INVENTION: Novel mlk Receptor Tyrosine Kinases
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/08493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match 7.5%; Score 76.5; E
Best Local Similarity 21.4%; Pred. No. 3.4;
Matches 43; Conservative 32; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A REGISTRAITON NUMBER: 32,724
REFERENCE/DOCKET NUMBER: G15234A
TELEPHONE: (617) 816-581
INFORMATION FOR SEQ ID NO: 19:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 3 PCT-US95-08493-21 Sequence 21, Application PC/TUS9508493
                                                                                                                                                                                                                                                                                                                                STREET: LEGAL AFFAIRS
STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: MA
                                                                         145 SDLCQGSMHSPCANDLFYSMT 165
                                                                                                              317 EYMAYGDL----NEFLRSMS 332
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IBM PC compatible
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amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
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PCT-US95-08493-19
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DB 2;
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Best Local Similarity 20.1%; Pred. No. 4.6;
Matches 44; Conservative 37; Mismatches
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Best Local Similarity 20.1%; Pred. No. 4.6;
Matches 44; Conservative 37; Mismatches
  PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 60/008,657
FILING DATE: 15-DEC-1995
ATTORNEY-AGENT INFORMATION:
NAME: CODERT, ROBERT J
REGISTRATION NUMBER: 36,108
REFERENCE/DOCKET NUMBER: REG 195A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 914-345-7721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MEIISS-KLFILLTLATSSLLTSNIFCA----
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; Patent No. 6413740
; GENERAL INFORMATION:
                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 869 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-644-271-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: HOMO sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-077-955-33
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LENGTH: 869
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Patent No. 5814478
GENERAL INFORMATION:
APPLICANT: Valenauela, et al.
TITLE OF INVENTION: NOVEL TYROSINE KINASE RECEPTORS; TITLE OF INVENTION: AND LIGANDS
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Regeneron Pharmaceuticals, Inc.
STREET: 777 Old Saw Mill Road
CITY: Tarrytown
          COMPOTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/374,834
FILING DATE: 19-JAN-1995
CLASSIFICATION 33
FILING DATE: 21-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: CODERT, ROBOTE 36,108
RESIDENCE/DOCKET UNMBER: 36,108
RESIDENCE/DOCKET UNMBER: 36,108
RESIDENCE/DOCKET UNMBER: 36,108
RELECOMMUNICATION NUMBER: 36,108
TELEPHONE: (914) 345-7721
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 869 amino acids
TYPE: Amino acids
TYPE: Amino acids
FORMADENNESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                69;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
7.4%; Score 75.5; Di
Best Local Similarity 20.1%; Pred. No. 4.6;
Matches 44; Conservative 37; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OMPRATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
FILING DATE: 10-MAY-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-374-834-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 10591
COMPUTER READABLE FORM:
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MEDIUM TYPE:
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87 NLPLRFGRNVQEERSAGATANLPLRSGRNMEVSLVRRV--PNLPQRFGRTTTAKSVCRML 144
                                                                                                               Gaps
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                                                                                             --- DELVMSNLHS 37
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498 ISIMSSFAIFVLLTITT-----LYCCRRRKQWKNKKRESAAVTLTTLPSELLLDRLHP 550
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Valentuela et al., David M.
TITLE OF INVENTION: NOVEL TYROSINE KINASE RECEPTORS AND LIGANDS
FILE REFERENCE: REG135-B-PCT-US
CURRENT APPLICATION NUMBER: US/09/077,955A
CURRENT FILING DATE: 1996-09-10
EARLIER APPLICATION NUMBER: PCT/US96/20696
EARLIER APPLICATION NUMBER: PCT/US96/20696
EARLIER APPLICATION NUMBER: 08/644,271
EARLIER APPLICATION NUMBER: 08/644,271
EARLIER APPLICATION NUMBER: 06/008,657
EARLIER FILING DATE: 1996-05-10
EARLIER FILING DATE: 1995-12-15
NUMBER OF SEQ ID NOS: 36
SOFTWARE: PALENTIN VET. 2.0
                                                69;
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Length 869;
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83 HSFANLPLRFGRNVQEERSAGATANLPLRS------GRNMEVSLVRRVPNLPQR-- 130
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                                                                                                                                                                                                                                                                                                                                                    DB 4; Length 1170;
                                                                                                                                                                                                                                                      53; Indels
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CORRESPONDENCE ADDRESS: ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: DOS
SOFWARE: FastSED for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/933,750C
FILIC DATE: September 23, 1997
                                                                                                                                                                                       ; Score 74.5; DE; Pred. No. 9.4; 33; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           157 ANDLFYSMTCQHQEIQNP-DQKQSRRLLFKKIDD 189
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Patent No. 5932442
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Hillman, Jennifer L.
Bandman, Olga
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NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               131 ---FGRTT-TAKSVCR----
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OPERATING SYSTEM: DOS
                                                                                                                                                                             Query Match
Best Local Similarity 22.9°
Matches 49; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 348 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION: APPLICANT: Lal, P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Palo Alto
                       ; LENGTH: 1170
; TYPE: PRT
; ORGANISM: Human
US-09-749-588-2.
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APPLICANT: CHANDRAMOLLISWARAN, IShwar et al
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: CLOOLIO68
CURRENT APPLICATION NUMBER: US/09/749,588
CURRENT FILING DATE: 2000-12-28
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
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                                           | : | : : | : : | | : : | | : : | | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | 
                                                                                                                        87 NLPLRFGRNVQEERSAGATANLPLRSGRNMEVSLVRRV--PNLPQRFGRTTTAKSVCRML 144
                                                                                                                                                                             605 MVAVKM---LKEEASADMQADF-----QREAALMAEFDNPNIVKLLGVCAVGKPMCLLF 655
38 KENYDKYS---EPR----GYPKGERSLNFEELKDWGP---KNVIKMSTPAVNKMPHS-FA 86
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Sequence 16, Application US/09594669

Fatent No. 6331424

APLICANT: Beraud, Christophe
APPLICANT: Beraud, Christophe
TITLE OF INVENTION: No. 6331424el motor proteins and methods for
TITLE OF INVENTION: No. 631424el motor proteins and methods for
TITLE OF INVENTION: their use
TITLE OF INVENTION: their use
CURRENT APPLICATION NUMBER: US/09/594,669

CURRENT FILING DATE: 1099-04-20

PRIOR APPLICATION NUMBER: US 09/114,464

PRIOR FILING DATE: 1999-04-20

PRIOR FILING DATE: 1999-05-18

NUMBER OF SEQ ID NOS: 16

SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14 LATSSLLTSNIF--CADELVMSN--LHSKE----NYDK-----YSEPRGYPKGERSLNF 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       150 GSMH----SPCANDL--FYSMTCQHQEIQNPDQKQSRRLLFKKIDDAELKQEK 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         :1 | | | ::|:: :: 171 EQVHSIRGSSSANPVNSVRRKSCLVKEVEKMKNRREE----KRAQNSEMRMKR 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 7.4%; Score 75; DB 4; Length 725; Best Local Similarity 21.0%; Pred. No. 4; Matches 49; Conservative 43; Mismatches 77; Indels
                                                                                                                                                                                                                                                                                           : | :: : | 656 EYMAYGDLNEFLRSMSPHTVCS--LSHSDLSMRAQVSSP 692
                                                                                                                                                                                                                                                   145 SDLCQG-----SMHSPCANDLFYSMTCQHQEIQNP 174
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US-09-749-588-2
; Sequence 2, Application US/09749588
; Patent No. 6423521
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US-09-594-669-16
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SEQ ID NO 16
LENGTH: 725
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76 PAVNKMPHSFANLPLRFGRNVQEERSAGATANLPLRSGRNMEVSLVRRVPNLPQRFGRTT 135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             136 TAKSVCRMLSDLCQG-SMHSPC------ANDLF--YSMTCQ------HQEIQN 173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels 41; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26 CADELVMSNLHSK-ENYDKYSEPRGYPKGERSLNFEELK------DWGPKNVIKMST 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Beraud, Christophe
APPLICANT: Baraud, Christophe
TITLE OF INVENTION: No. 6331424el motor proteins and methods for
TITLE OF INVENTION: their use
TITLE OF INVENTION: their use
FILE REFERENCE: 1042
CURRENT APPLICATION NUMBER: US/09/594,669
CURRENT APPLICATION NUMBER: US 09/295,612
PRIOR PILING DATE: 1999-04-20
PRIOR FILING DATE: 1999-04-20
PRIOR FILING DATE: 1999-05-18
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |:|: |:| :| :| :| ||||:| |:| ||||:| |:| |||:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| 
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Matches 37; Conservative 34; Mismatches 64;
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Patent No. 6331424
                                                          TOPOLOGY: linear

IMMEDIATE SOURCE:

LIBRARY: MUSCNOT01

CLONE: 118160

US-09-234-613-10
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                               STRANDEDNESS:
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214 RMKR 217
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US-09-594-669-14
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                                                                                                                                                                                                                                                                                                                                                                                                                           26 CADELVMSNLHSK-ENYDKYSEPRGYPKGERSLNFEELK------DWGPKNVIKMST 75
                                                                                                                                                                                                                                                                                                                                                           41;
                                                                                                                                                                                                                                                        Ouery Match
7.1%; Score 72.5; DB 2; Length 348;
Best Local Similarity 22.2%; Pred. No. 2.7;
Matches 42; Conservative 25; Mismatches 81; Indels 4
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APPLICANT: Hillman, Jennifer L.
APPLICANT: Bandman, Olga
APPLICANT: Bandman, Olga
APPLICANT: Au-Young, Janice
APPLICANT: Au-Young, Janice
APPLICANT: Corley, Henry
APPLICANT: Corley, Nell C.
APPLICANT: Corley, Nell C.
APPLICANT: Guegler, Karl J.
APPLICANT: Gregler, Rarl J.
APPLICANT: Gre
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APPLICATION NUMBER: US/09/234,613
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TELEPHONE: 415-855-0555
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/933,750
FILING DATE: September 23, 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 10, Application US/09234613
Patent No. 6132973
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
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TELEX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: MUSCNOT01
; CLONE: 118160
US-08-933-750C-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                174 PDQKQSRRL 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 230 TDMKYRNRV 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
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US-09-234-613-10
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us-09-831-758a-8.rai

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(212) 869-9741/8864
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APPLICANT: Hu, Shi-Xue
APPLICANT: Hu, Shi-Xue
APPLICANT: Benedict. William F.
ITILE OF INVENTION: Broad-Spectrum Tumor Suppressor Genes, Gene Products and
TITLE OF INVENTION: Methods for Tumor Suppressor Gene Therapy.
CORRESPONDENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                             ----GLPVQFGRY 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                374 YGHPNPPNEKSRKHRNKQLQMQQLQMQQLQQQQQQQYAQKTEADMRNSQYKPKLDPTSY 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---GSMHSPCANDLFY 162
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                                                                                                                                                                                                                                                                                                                                                                         82;
                                                                                                                                                                                                                                                                                                                              7.1%; Score 72; DB 4; Length 538; 18.2%; Pred. No. 5.9; tive 32; Mismatches 61; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/038,760
                  Sequence 23, Application US/09457040B
Patent No. 6387641
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Wellon, Steve
TITLE OF INVENTION: Crystallized P38 Complexes
FILE REFERENCE: VPI/98-11
CURRENT APPLICATON NUMBER: US/09/457,040B
CURRENT FILING DATE: 1999-12-08
NUMBER OF SEQ ID NOS: 41
SOFTWARE: PatentIn version 3.0
SEQ ID NO 23
LENGTH: 538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E-AYQHQTQQKYLQEQQKRQQQQKLQEQQLQEQQ 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                163 SMTCQHQEIQNPDQKQSRRLLFKKIDDAELKQEK 196
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1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---PNLPQRFGRTTTAKSVCRMLSDLCQ-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 3, Application US/08038760 Patent No. 5496731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: POISSANT, Brian M
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 74
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
                                                                                                                                                                                                                                                                                                                        Ouery Match 7.18,
Best Local Similarity 18.28,
Matches 39; Conservative
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MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: U.S.A.
ZIP: 10036-2711
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New York
                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Yeast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
STREET: 11
                                                                                                                                                                                                                                                                                          US-09-457-040B-23
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STATE:
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Sequence 3, Application US/08470091
Patent No. 591236
GENERAL INFORMATION:
APPLICANT: Xu, Hong-Ji
APPLICANT: Hu, Shi-Xue
APPLICANT: Hu, Shi-Xue
APPLICANT: Benedict, Milliam F.
TITLE OF INVENTION: Broad-Spectrum Tumor Suppressor Genes, Gene Products and
TITLE OF INVENTION: Methods for Tumor Suppressor Gene Therapy.
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                     .;
6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   92 FGRNVQEERSAGATANLPLRSGR---NMEVSLVRRVPNLPQRFGRTTTAKSVCRMLSDLC 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  49 GYPKGERSLNFEELK-------DWGPKNVIKMSTPAVNKMPHSFANLPLR 91
                                                                                                                                                                                                                                                             Query Match 7.1%; Score 72; DB 1; Length 816; Best Local Similarity 21.5%; Pred. No. 11; Matches 47; Conservative 23; Mismatches 63; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,091
FILING DATE: JUN-16-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      520 -----ATSAF-----QTQKPLKSTSLSLFYKKV 542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               149 QGSMHSPCANDLFYSMTCQHQEIQNPDQKQSRRLLFKKI 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY AGENT INFORMATION:
NAME: Poissant, Brian M
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 7409-025-999
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: New York
COUNTRY: U.S.A.
2IP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/038,760
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                         17 SSLLTSNIF-----CADELVMS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (212) 790-9090
TELEFAX: (212) 790-9090
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
TENTIFY 816 amin
JELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 816 amino acids
TYPE: AMINO ACID
TOPOLGS: 1:---
MOLEGY: 1:---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : 816 amino acids
amino acid
                                                                                                                                                                                  MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                    362 SKLLNDNIFHMSLLACALEVVMATYSRSTSQNLDSGTDLSFPWILNVLNLKAFDFYKVIE 421
                                                                                                                                                                                                                                                               ----NLHSKENYDKYSEPR 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: SHEPARD, H. M. APPLICANT: WEN, SHOW TO TITLE OF INVENTION: CHARACTERIZATION OF A NOVEL ANTI-PIIORB TITLE OF INVENTION: MONOCLONAL ANTIBODY NUMBER OF SEQUENCES: CORRESPONDENCE ADDRESS: CORRESPONDENCE ADDRESS: ADDRESS: TOWNSEND & TOWNSEND & CREW LLP
                                                                                         Score 72; DB 2; Length 816;
Pred. No. 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1; Length 928;
                                                                                                                                     63; Indels
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COUNTRY: U.S.A.

I 194111

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IEBM PC COMPATIBLE
COMPUTER: IEBM PC COMPATIBLE
OFFWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US-08/08/204,329
FILING DATE: 15-AUG-1994

**TELING DATE: 15-AUG-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                            149 QGSMHSPCANDLFYSMTCQHQEIQNPDQKQSRRLLFKKI 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             520 -----ATSAF-----QTQKPLKSTSLSLFYKKV 542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/05866
FILING DATE: 14-JUL-1992
ATTORNEY/AGENT INFORMATION:
NAME: RENEE A. FITTS
REGISTRATION NUMBER: 35,136
REGISTRATION NUMBER: 16930-000400US
TELECOMMUNICATION INFORMATION:
TELECPHONE: (415) 326-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: TOWNSEND & TOWNSEND & CREW LLP STREET: TWO EMBARCADERO CENTER, 8TH FLOOR
                                                                                    Query Match 7.1%; Score 72; DB Best Local Similarity 21.5%; Pred. No. 11; Matches 47; Conservative 23; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 7.1%; Score 72; DB Best Local Similarity 21.5%; Pred. No. 13; Matches 47; Conservative 23; Mismatches
                                                                                                                                                                           17 SSLLTSNIF-----CADELVMS----
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Sequence 1, Application US/08204329

Patent No. 5710255

GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 928 amino acids
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-470-091-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: SAN FRANCISCO
STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
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Gaps

96;

Indels

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92 FGRNVQEERSAGATANLPLRSGR----NMEVSLVRRVPNLPQRFGRTTTAKSVCRMLSDLC 148
                                                                                 DWGPKNVIKMSTPAVNKMPHSFANLPLR 91
 ----NLHSKENYDKYSEPR 48
                                                                                                                                                                                                              632 -----ATSAF-----QTQKPLKSTSLSLFYKKV 654
                                                                                                                                                                                         149 OGSMHSPCANDLFYSWTCQHQEIQNPDQKQSRRLLFKKI 187
                                                                                                                                                                                                                                                                    Search completed: March 26, 2003, 10:17:28 Job time : 32 secs
17 SSLLTSNIF-----CADELVMS--
                                                             49 GYPKGERSLNFEELK
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GenCore version 5.1.4_p5_4578

Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 26, 2003, 10:14:34; Search time 28 Seconds (without alignments) 923.935 Million cell updates/sec perfect score: US-09-831-758A-8

Perfect score: US-09-831-758A-8

Sequence: 1018
Sequence: 1028
Sequence: 1038
Searched: 613006 seqs, 131990659 residues
Total number of hits satisfying chosen parameters: 613006
Maximum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 10%
Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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/cgn2\_6/ptodata/1/paa/US07\_NEW\_COMB.

/cgn2\_6/ptodata/1/paa/US06

Pending\_Patents\_AA\_New:

Database :

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7	8		629	9	-10-369-493-200	
m		•	1817	9	-140 - 398	888
4	81.5	8.0	1358	9	-10 - 369	1658
S	81.5	8.0	1426	9	-10-322-579-15	15.00,
9	81.5	8.0	1435	9		2178
7	81	8.0	471	S	-09-724	74898.
00	81	8.0	471	ហ	US-09-724-676A-74898	
σ,	81	8.0	502	9	US-10-017-161-2042	
10	81	8.0	537	Ŋ	US-09-724-676-74897	74897
11	81	8.0	537	ഗ	-09-724	-
12	81	о. В	709	ហ	US-09-724-676-74919	74919,
13	81	0.	709	S	US-09-724-676A-74919	74919
14	81		713	Ŋ	US-09-724-676-74922	74922.
15	81		713	'n	US-09-724-676A-74922	74922.
10	81	٠	772	S	US-09-724-676-74921	74921.
17	81	٠	772	ß	-60	•
87	81	٠	1343	9	10-	
19	81	8.0	1351	9	282-	7514
20	80	٠	302	9	US-10-206-618-6	_
21	80	7.9	556	9	US-10-206-618-4	4
22	80	7.9	609	9	US-10-206-618-3	Sequence 3 Appli
23	80	7.9	609	9	10-	, -
24	80	7.9	1305	9	-10-	1100
25	79.5	7.8	509	9	-10-282-	
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US-10-282-122A-56549

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_	7.7	099	9	US-10-264-213-138	Sequence 138	8, App
78.5	7.7	662	9	US-10-264-213-232	Sequence 232	2, App
Ŋ	7.7	406	9	US-10-264-213-155	Sequence 155.	5. App
_	7.6	270	9	US-10-282-1228-60255		ď
_	7.6	1131	9	US-10-366-683-31247	Sequence 312	31247, A
76.5	7.5	1357	9	US-10-369-493-5432		5432. An
	7.5	899	9	US-10-369-493-4010		4010, Ap
75.5	7.4	460	S	US-09-724-676-82376		82376. A
	7.4	460	5	US-09-724-676A-82376		82376, A
10	7.4	725	S	US-09-849-602-20	Sequence 20.	Appl
	7.3	280	-	PCT-US03-03161-2		2. Appli
	7.3	280	ø	US-10-350-385-2		Appli
	7.3	490	-	PCT-US03-03161-4	4	Appli
	7.3	490	9	US-10-350-385-4	4	Appli
74.5	7.3	492	-	PCT-US03-03161-7	, ,	Appli
	7.3	492	ڡ	US-10-350-385-7	Seguence 7.	Appli
	7.3	538	S	US-09-724-676-74895		74895, A

## ALIGNMENTS

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US-10-202-122A-5649

Sequence 56549, Application US/10282122A
Sequence 56549, Application US/10282122A
Sequence 56549, Application US/10282122A
Sequence 56549, Application US/10282122A
APPLICANT: Wandor, Carlos
APPLICANT: Wandor, Carlos
APPLICANT: Wandor, Cheryl
APPLICANT: Tradick, John
APPLICANT: Wandoro, Robert
APPLICANT: Wandoro,
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APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Slater, Stewen C.
APPLICANT: Slater, Stewen C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
FILE REFERENCE: 38-10(52052)8
FILE REFERENCE: 38-10(52052)8
CURRENT PILING DATE: 2003-02-28
PRIOR PILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
                                                                                                                                                                                                                                                                                                                                                                                                                 987 VSLVDEFPSELSDSDRQIINEKM-QLLKDIFANNLKSAISNNFRESDIIILKGEIEDYPM 1045
                                                                                                                                                                                                                                                                                                                                                                                        74 STPAVNKMPHSF-----ANLPLRFGRNVQEERSAGATANLPLRSGRNMEVSLVRRVPNL 127
                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63 KDWGPKNVIKMSTPAVNKMPHSFANLPLRFGRNVQEERSAGA----TANLPLRSGRNME 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        940 K-----LSTIPTKSNRRVSHSDINSSK--PKNTKENLSKSSWRQEWLANLKL----IS 986
                                                                                                                                                                                                                                                                                                            28 DELVMSNLHSKENYDKYSEP------RGYPKGERSLNFEELKDWGPKNVIKM 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7 KLFILLTLATSSLLTSNIFCADELVMSNL----HSKENYDKYSEPRGYPKGERSLNFEEL 62
                                                                                                                                                                                                                                                                           39;
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                                                                                                                                                                                                                                   DB 6; Length 1817;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1358;
                                                                                                                                                                                                                                                                         64; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1632 PHTLNSTSTSKS----FQSTVTGELNAPYSKQFVHSKSSQYRKMK 1672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 118 VSLVRRVPNLPQRFGRTTTAKSVCRMLSDLCQGSMHSPCANDL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   128 PQRFGRTTTAKSVCRMLSDLCQGSMHSPCANDLFYSMTCQHQEIQ 172
                                                                                                                                                                                                                                                                                                                                                 1527 EDLVLSDISPKGVWDKILEPVACVRKKSEMLQLFPAYLKGE---
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                                                                                                                                                                                                                                 Score 83.5; DB
Pred. No. 34;
7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8.0%; Score 81.5; DE
23.2%; Pred. No. 39;
Live 34; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1658, Application US/10369493 GENERAL INFORMATION:
            PRIOR FILING DATE: 1999-04-02
PRIOR APPLICATION NUMBER: 60/127,607
PRIOR FILING DATE: 1999-03-31
                                                                                                                                                                                                                 8.2%; Su.
21.2%; Pred
27; }
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; ORGANISM: Saccharomyces cerevisiae
US-10-369-493-1658
                                                                        NUMBER OF SEQ ID NOS: 6322
SOFTWARE: CuraNator Version 1.0
SEQ ID NO 3988
                                                                                                                                                                                                                               Query Match
Best Local Similarity 21.23
Matches 35; Conservative
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Best Local Similarity
                                                                                                                                                                     ; ORGANISM: HOMO US-10-218-140-3988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-369-493-1658
                                                                                                                                LENGTH: 1817
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                                                                                                                                                     TYPE: PRT
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                                                                                                                                                         56 SLNF-----EELKDWGPKNVIK-----MSTPAVNKMPHSFANLPLRFGRNVQEERS 101
                                                                                                                                                                                        SGRNM-----EVSLVRRVPNLPQRFG-RTTTAKSVCR---MLSDLCQGSMHSPCAND 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             342 BADRLIN-QSFQGWCPKLMSHLKTDKLDTLP-----GNVIKMIFSATLTTNTEKL 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NGLNLYKPKLFLKQTDKLYQLPNKLNEFNINIPTAKSVYKPLILLYSICOFMAHSPIA-- 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          52 KGERSLNFEELKDWGPKNVIKMSTPAVNKMPHSFANLPLRFGRNVQEERSAGATANLPLR 111
                                                     Gaps
                                                                              1 MEIISSKLFILLTLATSSLLTSNIFCA----DELVMSNLHSKENYDKYSEPRGYPKGER 55
                                                                                                         44;
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SUBJURIAL AND CONTRACTORY:
APPLICANT: Leach, Martin D.
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES AND POLYPEPTIDES
TITLE OF INVENTION: ENCODED THEREBY
FILE REFERENCE: 15966-543 CON
CURRENT APPLICATION NUMBER: 02/10/218,140
CURRENT FILING DATE: 2002-08-12
PRIOR APPLICATION NUMBER: 09/540,763
PRIOR RILING DATE: 2000-03-30
PRIOR PLILING DATE: 1999-04-05
PRIOR FILING DATE: 1999-04-05
PRIOR FILING DATE: 1999-04-05
PRIOR PRICATION NUMBER: 60/127,636
      Score 97; DB 6; Length 931;
Pred. No. 0.84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 6; Length 629;
                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES CURRENT APPLICATION NUMBER: US/10/369,493 CURRENT FILING DATE: 2003-02-28 PRIOR APPLICATION NUMBER: US 60/360,039 PRIOR FILING DATE: 2002-02-21 NUMBER OF SEQ ID NOS: 47374 LENGTH: 629
                                               55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                160 LFYSMTCQHQEIQNPDQKQSRRLLFKKIDDAELKQEK 196
Query Match 9.5%; Score 97; DB 6 Best Local Similarity 27.3%; Pred. No. 0.84, Matches 38; Conservative 22; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match
8 3%; Score 84; DB
Best Local Similarity 21.7%; Pred. No. 9.5;
Matches 34; Conservative 28; Mismatches
                                                                                                                                                                                                                                                                                                                                                                              Sequence 2002, Application US/10369493 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Saccharomyces cerevisiae
US-10-369-493-2002
                                                                                                                                                                                                                                                                  119 YDETVYQVSLPTTQKQNLQ 137
                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
                                                                                                                                                                                                                                       102 AGAT --- ANLPLRSGRNME 117
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US-10-369-493-2002
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56 SLNFEELKDWGPKNVIKMSTPAVNKMP-HSFANLPLRFGRNVQEERSAGATANLPL--- 110
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                                                                                                                                                                            123 LRSRSTRMSTVSELRITAQENDMEVELPAAANSRKQFSVPPAPTRPSCPAVAEIPLRMVS 182
10 ILLTLATSSLLTSNIF--CADELVMSN--LHSKE----NYDK----YSEPRGYPKGER 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     146 DLCQGSMH----SPCANDL--FYSMTCQHQEIQNPDQKQSRRLLFKKIDDAELKQEK 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EEMEEQVHSIRGSSSANDVNSVRRKSCLVKEVEKMKNKREE----KKAQNSEMRMKR 235
                                                             77 AVNKMPHSFANLPLRFGRNVQEERSAGATANLPLRSG------RNMEV-----SL
                                                                                           794 GSDMLPAQQKMVPLPFGEHPQQEYGMGPRPFLPMSQGPGSNSGLRNLREPIGPDQRTNSR
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13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 74898, Application US/09724676A
; GRNERAL INFORMATION:
APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676A
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SEQ ID NO 74898
; LENGTH: 471
                                                                                                                                                                                                                                                                                                                                                                                         Sequence 74898, Application US/09724676
GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
SEQ ID NO 74898
LENGTH: 471
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13;
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8.0%; Score 81; DB 5
Best Local Similarity 21.1%; Pred. No. 13;
Matches 50; Conservative 44; Mismatches
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Pred. No.
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US-09-724-676A-74898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Homo sapiens
US-09-724-676-74898
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Best Local Similarity
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                                                             APPLICANT: BASLER, Konrad
APPLICANT: BRUNNER, Erich
APPLICANT: BRUNNER, Erich
APPLICANT: FROESCH, Barbara
APPLICANT: FROESCH, Barbara
APPLICANT: FREESCH, Oliver
TITLE OF INVENTION: ESSENTIAL DOWNSTREAM COMPONENT OF THE WINGLESS SIGNALING
FILE REFERENCE: 060361
CURRENT APPLICATION NUMBER: US/10/322,579
CURRENT APPLICATION NUMBER: US/09/915,543
PRIOR PLILNG DATE: 2000-07-27
PRIOR PLILNG DATE: 2000-07-27
PRIOR FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PATENTIAL NOS: 22
SOFTWARE: PATENTIAL NOS: 22
SOFTWARE: PATENTIAL NOS: 22
SOFTWARE: PATENTIAL NOS: 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    77 AVNKMPHSFANLPLRFGRNVQEERSAGATANLPLRSG------RNMEV-----SL 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Hyseq, Inc.
APPLICANT: Hyseq, Inc.
APPLICANT: Tang, Y, Tom et al
TILLE OF INVENTION: Novel Nucleic Acids and Polypeptides
FILE REFERENCE: 2127-2030
CURRENT APPLICATION NUMBER: US/10/276,774
CURRENT EILING DATE: 2002-11-18
PRIOR FILING DATE: 2000-04-27
PRIOR FILING DATE: 2000-04-27
PRIOR FILING DATE: 2000-04-27
PRIOR FILING DATE: 2000-02-03
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 8.0%; Score 81.5; D
Best Local Similarity 22.3%; Pred. No. 41;
Matches 41; Conservative 25; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----KGERSLNF-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2178, Application US/10276774 GENERAL INFORMATION:
US-10-322-579-15; Sequence 15, Application US/10322579; GENERAL INFORMATION:
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Best Local Similarity 22.3*
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US-10-322-579-15
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US-10-276-774-2178
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LENGTH: 1435
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56 SLNFEELKDWGPKNVIKMSTPAVNKMP-HSFANLPLRFGRNVQEERSAGATANLPL--- 110
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                                                                                                                                                                                                                                                                                                                         -----RVPNLPQRFGRTTTAKSVCRMLS 145
                                                                                                                                                                                                                                                                                 56 SLNFEELKDWGPKNVIKMSTPAVNKMP-HSFANLPLRFGRNVQEERSAGATANLPL---- 110
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                                                                                                         64; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        146 DLCQGSMH----SPCANDL--FYSMTCQHQEIQNPDQKQSRRLLFKKIDDAELKQEK 196
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                                              8.0%; Score 81; DB 5; Length 537;
21.1%; Pred. No. 16;
tive 44; Mismatches 79; Indels
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APPLICANT: Compugen LTD
FITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222; SOFWARE: Patentin version 3.2
SEQ ID NO 74919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 74897, Application US/09724676A
GENERAL INFORMATION:
APPLICANT: COMPUGEN LTD
TITLE OF INVENTION: Variants of alternative splicing
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CURRENT APPLICATION NUMBER: US/09/724,676A
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
SEQ ID NO 74897
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                                                                                Best_Local Similarity 21.1% Matches 50; Conservative
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US-09-724-676A-74897
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US-09-724-676A-74897
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US-09-724-676-74919
US-09-724-676-74897
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                                                                                                Gaps
                                                              10 ILLTLATSSLLTSNIF -- CADELVMSN -- LHSKE -- -- NYDK -- -- - YSEPRGYPKGER 55
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   64;
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      Indels
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GENERAL INFORMATION:
APPLICANT: SUWA, MAKIKO
APPLICANT: ASIA, KIYOSHI
APPLICANT: ARIYAMA, YUTRKA
APPLICANT: ABURATANI, HIROYUKI
TITLE OF INVERTION: NOVEL G PROTEIN-COUPLED RECEPTORS
FILE REFERENCE: 084335/0152
CURRENT APPLICATION NUMBER: US/10/017,161
CURRENT FILING DATE: 2002-12-18
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TITLE OF INVENTION: Variants of alternative splicing
FILLE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTHARE: Patentin version 3.2
SEQ ID NO 74897
LENCTH: 537
      79;
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8.0%; Score 81; DB

Best Local Similarity 31.1%; Pred. No. 14;

Matches 38; Conservative 15; Mismatches
      Mismatches
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PRIOR APPLICATION NUMBER: JP 2001/246789
PRIOR FILING DATE: 2001-06-18
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GENERAL INFORMATION:
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2042
LENGTH: 502
         Conservative
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GOGANISM: Homo sapiens
US-10-017-161-2042
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                                                                                                                       Gaps
                                                                                                                                                                                  LTLRMAMDSSLQARLFPGLAIKIQRSNGLIHSANVRTVNLEKSCVSVEWAE-GGATKG-K 70
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                                                                                                                                                                                                                                                                                                                                                                                                                                   183 EEMEEQVHSIRGSSSANPVNSVRRKSCLVKEVEKMKNKREE----KKAQNSEMRMKR 235
                                                                                                                     64;
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                                                                        ; Score 81; DB 5; Length 709;
; Pred. No. 21;
44; Mismatches 79; Indels
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GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
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TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICANTON NUMBER: US/09/724,676A
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
SOFTWARE: Patentin version 3.2
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21.1%; Pred. No. 3
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                                                                                                                                                                                                                                                                                                                             111 ---RSGRNMEVSLVR-----
                                                                            Query Match 8.0%;
Best Local Similarity 21.1%;
Matches 50; Conservative 4
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ORGANISM: Homo sapiens
US-09-724-676A-74919
TYPE: PRT
ORGANISM: Homo sapiens
US-09-724-676-74919
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US-09-724-676A-74919
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 71 EIDFDDVAAINPE-----LLQLLPLHPKTNLPLQENVTIQKOKRRSVNSKIPAPKES 122
                                                                                                                                                                                                                                                                                        SLNFEELKDWGPKNVIKMSTPAVNKMP-HSFANLPLRFGRNVQEERSAGATANLPL--- 110
                                                                                                                                                                                                                                                                                                                EIDFDDVAAINPE-----LLQLLPLHPKTNLPLQENVTIGKQKRRSVNSKIPAPKES 122
                                                                                                                                                                                                                                                                                                                                                                                        10 ILLTLATSSLLTSNIF -- CADELVMSN -- LHSKE---- NYDK ----- YSEPRGYPKGER 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13 LTLRMAMDSSLOARLEPGLAIKIORSNGLIHSANVRTVNLEKSCVSVEWAE-GGATKG-K 70
                                                                                                                                                                                                              10 ILLTLATSSLLTSNIF--CADELVMSN--LHSKE----NYDK-----YSEPRGYPKGER 55
                                                                                                                                                                                                                                           146 DLCQGSMH----SPCANDL--FYSMTCQHQEIQNPDQKQSRRLLFKKIDDAELKQEK 196
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                                                                                                                                                                                                                                                                                                                                                                                                                                         DLCQGSMH----SPCANDL--FYSMTCQHQEIQNPDQKQSRRLLFKKIDDAELKQEK 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 713;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 74922, Application US/09724676A
GENERAL INFORMATION:
GENERAL INFORMATION:
TAPLICANT: Compugen LTD
TITLE OF INVENTION UNDERSE: US/09/724,676A
CURRENT FILION NUMBER: US/09/724,676A
CURRENT FILION DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
LENGTH: 713
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Pred. No. 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     44; Mismatches
                                                                                                                                           ; Score 81; DB
; Pred. No. 21;
44; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Search completed: March 26, 2003, 10:23:27 Job time : 31 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8.0%;
           SOFTWARE: Patentin version 3.2 SEQ ID NO 74922 LENGTH: 713
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illarity 21.1%;
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Best Local Similarity 21.18
Matches 50; Conservative
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NUMBER OF SEQ ID NOS: 97222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Homo sapiens
US-09-724-676A-74922
                                                                                        ; ORGANISM: Homo saplens
US-09-724-676-74922
                                                                                                                                                             Local Similarity
es 50; Conserve
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US-09-724-676A-74922
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                                                                        TYPE: PRT
                                                                                                                                                                                    Matches
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GenCore version  $5.1.4\_p5\_4578$  Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on:

March 26, 2003, 10:12:39; Search time 43 Seconds (without alignments) 438.194 Million cell updates/sec

US-09-831-758A-8 1018 1 MEIISSKLFILLTLATSSLL..........KQSRRLLFKKIDDABLKQEK 196 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283224 seqs, 96134422 residues Searched:

283224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

PIR\_73:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	notodi rosa	hypothetical prote		probable peptidase	probable peptidase	exodeoxyribonuclea		hypothetical prote	O	hypothetical prote	SIR4 protein - yea	cell division prot	DNA-directed DNA p	DNA-directed DNA p		probable cell divi	50S ribosomal prot	probable oxidoredu	maturation (pIVa2)	maturation (pIVa2)	hypothetical rhol	myosin heavy chain	hypothetical prote	NADH2 dehydrogenas	hypothetical prote	maturation (pIVa2)	oxidoreductase, GM	RND divalent metal	13,	keratin 13, type I
	£	10	C96804	A64903	C90891	F85726	D64116	T32984	863369	JE0366	T25206	A29360	AF0611	S19661	T43266	T40242	AB0168	G90573	D95408	Q4ADA5	Q4ADA2	T41523	A45627	S55957	T13248	T19918	Q4ADA7	н87451	E83330	A37343	KRHU3
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dР	Query	March	9.6	9.5	9.4	9.4	8.5	8.4	8.3	8.2	8.1	8.0			7.9	7.9	7.9	7.8	7.8	7.8	7.8	7.8	7.8	7.8	7.7	7.7	7.6	7.6	7.6	7.5	7.5
	0,000	91006	86	97	96	96	86.5	85.5	84	83.5	82	81.5	81	80	80	80	80	79.5	79.5	79.5	79.5	79.5	79.5	79	78.5	78	77	77	77	76.5	76.5
	Result		-	7	e	4	2	9	7	8	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

RESULT 2 A64903 probable zinc proteinase yddc (EC 3.4.99.-) - Escherichia coli (strain K-12) C;Species: Escherichia coli

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probable obtusifol	nypornerical proce	conserved hypothet	hypothetical prote	hypothetical prote	drought-inducible	hypothetical prote	ABC transporter AT	calmodulin-binding	probable ABC trans	obtusifoliol 14-al	gag-like protein -	hypothetical prote	complement compone	myosin heavy chain	NADH2 dehydrogenas
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76.5	76.5	16	16	75.5	75.5	75.5	75	75	75	74.5	74.5	74.5	74.5	74.5	74
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

# ALIGNMENTS

A; Cross-references: 1-426 <sto> A; Cross-references: GB:AE005173; NID:g6382497; PIDN:AAF07783.1; GSPDB:GN00141 C; Genetics: A; Gene: T9416.8 A; Map position: 1 C; Superfamily: cytochrome-c peroxidase Query Match Best Local Similarity 29.3%; Pred. No. 0.16; Matches 53; Conservative 20; Mismatches 66; Indels 42; Gaps 11; Matches 53; Conservative 20; Mismatches 66; Indels 42; Gaps 11; Oy 2 EIISSKLFILLTLATSSLLTSNIFCADELVMSNLHSKENYDKYSEPRGYPKGERSLN 58 ::  :                                 </sto>
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exodeoxyrinourcleaser vision included incomparation included in the exodeoxyrinourcleaser vision 18-Aug-1995 #text_change 08-Oct-1999 (Species: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 08-Oct-1999 (Species: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 08-Oct-1999 (Species: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 08-Oct-1999 (Species: 18-Aug-1995 #sequence, revision 18-Aug-1995 #text_change 08-Oct-1999 (Species: 1995 #text_change, revision 19-Billey, revoleoxyribonuclease v 135K chain
exodeoxyribonuclease V 135K chain homolog - Haemophilus influenzae (strain Rd KW20)
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8.5%; Score 86.5; DB 2;
Best Local Similarity 20.9%; Pred. No. 7.4;
Matches 39; Conservative 33; Mismatches 80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 9.4%; Score 96; DB 2;
Best Local Similarity 27.3%; Pred. No. 0.65;
Matches 38; Conservative 22; Mismatches
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119 YDETVYQVSLPTTQKQNLQ 137
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                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-931 <BLAT>
A; Residues: 1-931 <BLAT>
A; Cross-references: GB: AE000246; GB: U00096; NID: 91787764; PIDN: AAC74567.1; PID: 91787770;
A; Experimental source: strain K-12, substrain MG1655
C; Genetics:
A; Genetics:
A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; 
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                            C;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 01-Mar-2002
C;Accession: A64903
R;Blattner, F.R; Plunkett III, G; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; 6.A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Teference number: A64720; MUID:97426617; PMID:9278503
A;Accession: A64903
A;Status: nucleic acid sequence not shown; translation not shown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SLNF-----EELKDWGPKNVIK-----MSTPAVNKMPHSFANLPLRFGRNVQEERS 101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 931;
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Best Local Similarity
Matches 38; Conserva
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A;Experimental source: clone T23G7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary
A;Molecule type: mark
A; Residues: 1-1163 <COL>
A;Cross-references: GB:AF085184; NID:93820579; PIDN:AAC95469.1; PID:93820580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tight junction protein, ZO-2 - chicken
C; Species: Gallus gallus (chicken)
C; Species: Gallus gallus (chicken)
C; Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 21-Jul-2000
C; Accession: JE0366
R; Collins, J.R.; Rizzolo, L.J.
Biochem. Biophys. Res. Commun. 252, 617-622, 1998
A; Title: protein-binding domains of the tight junction protein, ZO-2, are his A; Reference number: JE0366; MUID:99037550; PMID:9837755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein T23G7.5 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T25206
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                                                                                                                                                                                                            112 SGRNM-----EVSLVRRVPNLPQRFG-RTTTAKSVCR---MLSDLCQGSMHSPCAND 159
                                                                                                                                                                                                                                          KGERSLNFEELKDWGPKNVIKMSTPAVNKMPHSFANLPLRFGRNVQEERSAGATANLPLR 111
                                                                                                                                        342 EADRILN-QSFQGWCPKILMSHLKTDKLDTLP------GNVIKMIFSATLTTNTEKL 390
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                                                         44;
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     Length 629;
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----AKILIFVKSNESSIRLSK 466
                                                                                                                                                                                                                                                                                                                      160 LEYSMTCQHQEIQNPDQKQSRRLLFRKIDDAELKQEK 196
          DB 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 8.2%; Score 83.5; 1
Best Local Similarity 27.6%; Pred. No. 14;
Matches 24; Conservative 17; Mismatches
                                                           28; Mismatches
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26.0%; Pred. No.
        8.3%; Score 84;
21.7%; Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               101 SAGATANLPLRSGRNMEVSLVRRVPNL 127
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A; Introns: 56/2; 137/2; 170/1; 207/1
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Best Local Similarity 26.0%
Matches 38; Conservative
          Query Match 8.3%
Best Local Similarity 21.7%
Matches 34; Conservative
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A; Residues: 1-261 <W
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Introns: 51/1; 103/1; 188/3; 304/2; 339/2; 392/3; 448/2; 545/3; 646/3; 794/3; 910/2
                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA A; Molecule type: DNA A; Residues: 1-1015 <- COLOR A; Residues: 1-1015 <- COLOR A; Cross - references: EMBL: AF045645; PIDN: AAC02607.1; GSPDB:GN00022; CESP: K02D7.4 A; Experimental source: strain Bristol N2; clone K02D7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein YNR038w - yeast (Saccharomyces cerevisiae)
N.Alternate names: hypothetical protein N3302
C; Species: Saccharomyces cerevisiae
C; Species: Saccharomyces cerevisiae
C; Species: Saccharomyces cerevisiae
C; Species: Sa3369
R; Pohl, T.M.
submitted to the Protein Sequence Database, April 1996
A; Reference number: S63346
A; Accession: S63369
                                                                                                                                                Species: Caenorhabditis elegans
Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ---GSMHSPCANDLFYSMTCQHQ------EIQNPDQK 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             641 KKIGAPLTHKLIKLFRNTCSOETPTSHSOLAIDILLKCVPDHONVATLILRTETLNPDDQ 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      :: || ::|
522 ATVLNKRCEASTSSLNSCNKGKETIVNKFITDLTAGGVEVRVLEVLENIFIFGSYTFAKK 581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FGRNVQEERSAGATANLPLRSGRNMEVSLVRRVPNLPQRFGRTTTAKSVCRMLSDLCQ-- 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12 LTLATSSLLTSNIFCADELVMSNLHSKENYDKYSEPRGYPKGERSLNFEELKDWGPKNVI 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1015;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                 R;Du, Z.; Maggi, L.
submitted to the EMBL Data Library, February 1998
A;Description: The sequence of C. elegans cosmid K02D7.
A;Reference number: 221259
A;Stetus: prellminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Gene: SGD:DBP6
A;Cross-references: SGD:S0005321: MIPS:YNR038w
A;Hap position: 14R
C;Superfamily: fruit fly gene Dbp73D protein
C;Superfamily: fruit fly gene Dbp73D protein
C;Keywords: ATP; nucleotide binding; P-loop
F;334-241/Region: nucleotide-binding motif B
F;331-342/Region: nucleotide-binding motif B
F;341-344/Region: DEAD motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94;
                                                                                                                          hypothetical protein K02D7.4 - Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8.4%; Score 85.5; DI
19.8%; Pred. No. 7.4;
Live 35; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            178 OSRRLLFKKIDDA----ELKQE 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A: Wolecule type: DNA
A: Residues: 1-629 <POH>
A; Cross references: EMBL:271653; NI
A: Experimental source: strain 5288C
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  72 ------KMSTPAVN------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 19.8
Matches 52; Conservative
1070 REHFDVE 1076
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Gene: CESP: K02D7.4
                                                                                                                                                                                                         C; Accession: T32984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Map position: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               101
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C. Species: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
C;Species: Species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001
C;Accession: AF0611
C;Accesion: AF0611
C;Accession: AF0611
C;Accession: AF0611
C;Accession: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cincession: S19661
R. Pignade, G.; Bouvier, D.; de Recondo, A.M.; Baldacci, G.
J. Mol. Biol. 222, 209-218, 1991
A;Title: Characterization of the PoL3 gene product from Schizosaccharomyces pombe in A; Reference number: S19661; MUID:92071954; PMID:1960723
A;Accession: S19661
A;Molecule type: DNA
A;Residues: 1-1084 <PIG>
A;Cross-references: EMBL:X59278; NID:95010; PIDN:CAA41968.1; PID:95011
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA-directed DNA polymerase (EC 2.7.7.7) III large chain - fission yeast (Schizosacciscosaccharomyces pombe
C;Species: Schizosaccharomyces pombe
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Residues: 1-1343 <PAR>
A;Cross-references: GB:AL513382; PIDN:CAD05360.1; PID:916502124; GSPDB:GN00176
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   65 WGPKNVIKMSTPAVNKMPH----SFANLPLRFGRNVQE-----ERSAGATANLPLRS 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            71 IKMSTPAVNKMPHSFANLPLRFGRNVQEERSAGATANLPLRSGR------NMEVSLVR 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          123 R----VPNLPQRFGRTTTAKSVCRMLSDLCQGSMHSP--CAN---DLFYSMTCQHQEIQN 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1171 QRPSVDVITGLIK--ANIPTRIAFTVSSKIDSRTILD--QGGAESLLGMGDMLYS 1221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               113 GR---NMEVSLVRRVPNLPQRFGRTTTAKSVCRMLSDLCQGSMHSPCA-NDLFYS 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       42;
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C; Superfamily: herpesvirus DNA-directed DNA polymerase
C; Keywords: DNA binding; nucleotidyltransferase; nucleus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8.0%; Score 81; DB 2;
25.2%; Pred. No. 29;
tive 24; Mismatches 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ed. No. 27;
Mismatches
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                                                                            165 TCQ----HQEIQN-PDQKQSRRLLFKK 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 25.2%
Matches 29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            174 PDQKQSRRLLFKKIDD 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Accession: AF0611
A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Gene: STY0958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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A; Residues: 1-1358 <AMR>>
A; Cross-references: GB:M37249; NID:9531115; PIDN:AAA20881.1; PID:9531116
R; Davies, C.J.; Hutchison III, C.A.
R; Davies, C.J.; Hutchison III, C.A.
S. Davies, C.J.; Butchison III, C.A.
A; Description: Tn3 transposon/deletion sequencing of a 9.4kb DNA fragment: Characterisat
A; Reference number: S47932
                                                                                                                                                                                                                                                                                                                                                                                                                                                            N.Alternate names: protein YD934.12; protein YDR227w; STE9 protein C;Species: Saccharomyces cerevisiae C;Species: Saccharomyces cerevisiae C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 21-Jul-2000 C;Accession: A29360; S47935; S5944; S53988; S47476; S47950 R;Marshall, M.; Mahoney, D.; Rose, A.; Hicks, J.B.; Broach, J.R. A) Mahoney, D.; Rose, A.; Hicks, J.B.; Broach, J.R. A;Title: Functional domains of STR4, a gene required for position effect regulation in A;Reference number: A29360; MUID:88142836; PMID:3325825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: EMBL:U13239; NID:9532747; PIDN:AAC33144.1; PID:9532751
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ٠<u>.</u>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  940 K-----LSTTPTKSNRRVSHSDTNSSK--PKNTKENLSKSSWRQEWLANLKL----IS 986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          118 VSLVRRVPNLPQRFGRTTTAKSVCRMLSDLCQGSMHSPCANDL------FYSM 164
                                                                                                                          67 IDGTRFVPFKTP----LÖSSFFD-----GKNMPVELQFGVKTLISLAQQANKQIGLVIDL 117
                                                                        70 V----IKMSTPAVNKMPHSFANLPLRFGRNVQEERSAGATANLPLRSGRNMEVSLVRRV 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-1358 cAUR>
A; Residues: 1-1358 cAUR>
A; Cross references: EMBL:248612; NID:9728671; PID:9728683; MIPS:YDR227w
A; Cross references: EMBL:248612; NID:9728671; PID:9728683; MIPS:YDR227w
A; Experimental source: strain AB972
R; Davies, C.J.; Hutchison III, C.A.
Richers Res. 23, 507-514, 1995
A; Title: Insertion site specificity of the transposon Tn3.
A; Reference number: S53985; MUID:95192063; PMID:7885847
A; Reference number: S53988
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13 LNLSHSILI--SIFSVS--VMSNYHHNHNYQ--HRPRGYERLPGKRLPDRWNIYDNVGRD
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A, Molecule type: DNA
A, Residues: 1-993,'L', 995-1358 <DAV>
A, Cross-references: EMBL:L35344; EMBL:U3239; EMBL:236548
R; Murphy, L.; Harris, D.
Submitted to the EMBL Data Library, March 1995
A; Reference number: $59423
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23.2%; Pred. No. 26;
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C;Keywords: DNA binding; transcription regulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34; Mismatches
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A)Cross-references: SGD:S0002635; MIPS:YDR227w
                                                                                                                                                                                                                                                                    118 TNTDRYYKKTEWADHGVKYLKLNCPG 143
                                                                                                                                                                                                                      125 PNLPQRFGRTTTAKSVCRMLSDLCQG 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Molecule type: DNA
Residues: 1-993,'L',995-1358 <DAW>
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Matches 48; Conserv
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Search completed: March 26, 2003, 10:16:54
Job time : 48 secs
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Matches
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C; Species: Schizosaccharomyces pombe
C; Species: Schizosaccharomyces pombe
C; Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jan-2000
C; Accession: T40242
R; Bock, A.; Reinhardt, R.; McDougall, R.C.; Rajandream, M.A.; Barrell, B.G. submitted to the EMBL Data Library, October 1999
A; Reference number: 221916
A; Residue: T40242
A; Residue: T40242
A; Residue: 14086 < CORP
A; Residue: 1-1086 < CORP
A; Residue: 1-1086 < CORP
A; Cross references: EMBL: AL121815; PIDN: CAB58156.1; GSPDB: GN00067; SPDB: SPBC336.04
A; Experimental source: strain 972h-; cosmid c336
A; Conetics:
                                                                                                                                               MAN-directed DNA polymerase (EC 2.7.7.7) delta chain - fission yeast (Schizosaccharomyce NA-directed DNA polymerase delta

C; Species: Schizosaccharomyces pombe
C; Species: Schizosaccharomyces pombe
C; Date: 11.5da-7000 % sequence_revision 11.5da-2000 % text_change 21.5dl-2000
C; Accession: T43266
R; Pignede, G.; Bouvier, D.; de Recondo, A.M.; Baldacci, G.
R; Pignede, G.; Bouvier, D.; de Recondo, A.M.; Baldacci, G.
A; Title: Characterization of the POL3 gene product from Schizosaccharomyces pombe indica A; Reference number: 819661; MUID: 92071954; PMID: 1960723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                123 R----VPNLPQRFGRTTTAKSVCRMLSDLCQGSMHSP--CAN---DLFYSMTCQHQEIQN 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              123 R----VPNLPQRFGRTTTAKSVCRMLSDLCQGSMHSP--CAN---DLFYSMTCQHQEIQN 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              71 IKMSTPAVNKMPHSFANLPLRFGRNVQEERSAGATANLPLRSGR------NMEVSLVR 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-1086 <PIG>
A; Cross-references: EMBL:L07734; NID:g173383; PIDN:AAA35303.1; PID:g173384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   42;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Gene: pold
A;Introns: 77.1
C;Superfamily: herpesvirus DNA-directed DNA polymerase
C;Keywords: DNA binding; DNA replication; nucleotidyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1086;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Superfamily: herpesvirus DNA-directed DNA polymerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7.9%; Score 80; DB 2;
27.9%; Pred. No. 27;
tive 20; Mismatches 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1073 ---- QSVDLL-KRFDE 1083
1071 ----QSVDLL-KREDE 1081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 7.9%
Best Local Similarity 27.9%
Matches 38; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        174 PDQKQSRRLLFKKIDD 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Gene: SPDB:SPBC336.04
A;Map position: 2
A;Introns: 77/1
C;Superfamily: hernewit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 14
T40242
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C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001
C;Accession: AB0168
C;Accession: AB0168
C;Accession: AB0168
Geno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Douga il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Ba Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1305 <KUR>
A;Crosidues: 1-1305 <KUR>
C;Genetics:
                                                                                                                                                                                                                                                                        probable cell division protein ftsk [imported] - Yersinia pestis (strain C092)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          65 WGPKNVIKMSTPAVNKMPH-----SFANLPLRFGRNVQE-----ERSAGATANLPLRS 112
1021 RQVAQVNDLEVRFARLWTQ----CQRSMHQDVICTSRDCPIFYMRIAEHKKLQ- 1072
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         113 GR---NMEVSLVRRVPNLPQRFGRTTTAKSVCRMLSDLCQGSMHSPCA-NDLFY 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1305;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7.9%; Score 80; DB 2; Le. Local Similarity 25.4%; Pred. No. 34; les 29; Conservative 24; Mismatches 41;
                                                                                                                                     1073 ----OSVDLL-KRFDE 1083
                                                                                       174 PDQKQSRRLLFKKIDD 189
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us-09-831-758a-8.rsp

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GenCore version 5.1.4\_p5\_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
```

OM protein - protein search, using sw model

March 26, 2003, 10:08:54; Search time 26 Seconds (without alignments) 312.668 Million cell updates/sec Run on:

US-09-831-758A-8 1018 1 MEIISSKLFILLTLATSSLL.........KQSRRLLFKKIDDAELKQEK 196 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

112892 seqs, 41476328 residues Searched:

112892 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_40:\* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		p31828 escherichia		P54705 dictyosteli	••		schizo	human		saccha	human	human	homo					Q59105 alcaligenes	_	Q10172 schizosacch		-	-	_						-	-		0139	Q10432 schizosacch
SUMMARIES	ID	POOL ECOLI	EX5B_HAEIN	SNWA_DICDI	DBP6_YEAST	SIR4_YEAST	DPOD_SCHPO	PIV2_ADE02	PIV2_ADE05	YL01_YEAST	PIV2_ADE07	PIV2_ADE40	K1CM_HUMAN	MCAK_HUMAN	CP51_SORBI	MYSB_CAEEL	PDI1_MOUSE	NOSZ_ALCEU	AC15_MOUSE	YAV1_SCHPO	CP51_WHEAT	SYM_ARATH	T2C9_CITFR	K1CM_MOUSE	MESJ_BUCAI	YD71_SCHPO	CK11_YEAST	RB_HUMAN	RRPO_LYCVA	YAH2_YEAST	FAB1_CAEEL	RS4_BACST		YDD7_SCHPO
	DB	-	7	-	-	Н	-	-	H	-		-	Н	-	٦		-		-	Н	-	-		-	7	-	Н	Н	٦	-	-	٦	-	7
		931	1211	685	629	1358	1086	449	449	609	448	446	458	725	492	1966	662	643	1131	1794	453	797	330	437	440	720	538	928	2210	539	161	198	344	735
	% Query Match Length	9.5	8.5		8.3	٠	•	7.8	7.8	7.8	7.6	7.5	7.5	7.4	7.3	7.3	7.3	7.2	7.2	7.2	7.2	•		7.1	7.1	7.1			7.1	•	٠	7.0	7.0	•
	Score	97	86.5	84.5	84	81.5	80	79.5	79.5	79	77	76.5	76.5	75	4	74.5	74	73.5	•	ന	73	73	72.5	72.5	. 72.5	72.5	72	72	72	71.5	7.1	7.1	71	7.1
	Result No.		7	٣	4	2	9	7	8	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	78	29	30	31	32	33

000507 h probable	Q01036 herpesvirus	062954 picea ables	062940 pinus thunb	042698 catharanthu	P49997 azotobacter	Q9u9i5 drosophila	014186 schizosacch	P75157 mycoplasma	P23645 drosophila	P22338 louping ill	O54827 mus musculu
FAFY_HUMAN	VG51_HSVSA	RK2_FICAB	RK2_PINTH	GGPP_CATRO	RECF_AZOVI	SWA_DROPS	YDSB_SCHPO	Y43E_MYCPN	BIB DROME	POLG_LIV	A10A_MOUSE
=		Н	Н	-	-	Н		-	-	-	-
2555	269	275	276	357	364	529	846	300	700	980	1508
7.0	6.9	6.9	6.9	6.9	6.9	6.9	6.9	6.9	6	6.9	6.9
7.1	70.5	70.5	70.5	70.5	70.5	70.5	70.5	2.0	70	20	70
34	3.5	9 6	37	. ee	0 6	40	4.1	42		44	45

# ALIGNMENTS

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SEQUENCE 1211 AA; 139857 MW;
                                                                                                                                                                                                                       DNA repair; Complete proteome.
NP BIND 22 29 A
                                                                                                                          EMBL; U32811; AAC22966.1; -.
                                                                                                                                                                                                                                                                                            39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                          HSSP; P09980; 1UAA.
FIGR; H11321; -.
 SIMILARITY)
                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 39; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : | :::
1070 REHFDVE 1076
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID-44689;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          166 CQHQEIQ 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dictyostelium.";
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P54705;
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                                                                                                                                                                                                                                                                                                                    56 SLNF-----EELKDWGPKNVIK-----MSTPAVNKMPHSFANLPLRFGRNVQEERS 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PEDLINE 3780 ATCC 51907;

MEDLINE=95350630; PubMed=7542800;
Fleischman R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
Rerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
                                                                                                                                                                                                                                                                       1 MEIISSKLFILLTLATSSLLTSNIFCA-----DELVMSNLHSKENYDKYSEPRGYPKGER 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CATALYTIC ACTIVITY: Exonucleolytic cleavage (in the presence of ATP) in either 5'- to 3'-or 3'- to 5'-direction to yield 5'-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
Haemophilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       phosphooligonucleotides.
SUBUNIT: CONSIST OF THREE SUBUNITS; RECB, RECC AND RECD
                                                                                                                                                                                                           DB 1; Length 931;
                                                                                                     Oprotease; Zinc; Complete proteome.
80 ZINC (BY SIMILARITY).
84 ZINC (BY SIMILARITY).
84 ZINC (BY SIMILARITY).
160 ZINC (BY SIMILARITY).
360 A -> V (IN REF. 1).
867 L -> V (IN REF. 1).
67 LO4656 MW; 94A340CA83DB6DIE CRC64;
                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                  55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Exodeoxyribonuclease V beta chain (EC 3.1.11.5).
                                                                                                                                                                                                           9.5%; Score 97; DB 1; larity 27.3%; Pred. No. 0.15; Conservative 22; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT; 1211 AA
EMBL; X71917; CAA50734.1; ALT_FRAME.
EMBL; X71917; CAA50735.1; ALT_FRAME.
EMBL; AE000246; AAC74567.1; -
EMBL; D90791; BAA15164.1; ALT_INIT.
MEROPS; M16.UPB; -
                                                                  InterPro; IPR001431; Peptidase_M16.
Pfam; PF00675; Peptidase_M16; 1.
PR0SITE: PS00143; INSULINASE; 1.
                                                                                                                                                                                                                                                                                                                                                    ' 102 AGAT --- ANLPLRSGRNME 117
                                                                                                                                                                                                                                                                                                                                                                         119 YDETVYQVSLPTTQKQNLQ 137
                                                                                                        Hydrolase; Metalloprotease;
                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                         EcoGene; EG11744; pqqL.
InterPro; IPR001431; Pe
                                                                                                                                                                                                                       Local Similarity
hes 38; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=727;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RECB OR HI1321.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Venter J.C.:
                                                                                                                                                                                                                                                                                                                                                                                                                                    EX5B_HAEIN
                                                                                                                             ACT_SITE
METAL
                                                                                                                                                               CONFLICT
                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                            Query Match
                                                                                                                   METAL
                                                                                                                                                                                                                                  Matches
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@libersib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR004586; RecB.
InterPro; IPR00212; UvrD-helicase.
InterPro; IPR008212; UvrD-helicase.
InterPro; ITGR0609; recB: 1.
Hydrolase; Nuclease; Exonuclease; Endonuclease; Helicase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1014 IDKLRQSLQLDETFTESLQNWLQQISHTPLSNEIGIALADLA----NKDCIKEMPFYLAI 1069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         107 NLPLRSGRNMEVSLVRRVPNLPQRFGRTTTAKSVCRMLSDLCQGSMHSPCANDL-FYSMT 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              56 SLNFEELKDWGPKNVIKMSTPAVNKMPHSFANLPL------RFGRNVQEERSAGATA 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11 LLTLATSSLLTSN-IFCADELV-------MSNLHSKENYDKYSEPRGYPKGER 55
SIMILARITY: BELONGS TO THE HELICASE FAMILY. UVRD SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8.5%; Score 86.5; DB 1; Length 1211; 20.9%; Pred. No. 2.3; Live 33; Mismatches 80; Indels 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The homolog of chromatin binding protein Bx42 identified in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-97128797; PubMed-8973337;
Folk P., Puta F., Krpejsova L., Blahuskova A., Markos A.,
Rabino M., Dottin R.P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATP (POTENTIAL).

IM; 37B76430651FAD68 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dictyosfelium discoideum (Slime mold).
Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
SNWA protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            685 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gene 181:229-231(1996).
-!- SIMILARITY: BELONGS TO THE SNW FAMILY.
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RESULT 5
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                                                                                                                                                                          10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no wa
                                                                                                                                                                                                                                                                                                                123 KHEA-ILGE--KGSLHSQ-YKDLIPKQHTEH-ELQRPDDDELQETLDRTKNALEKIVNGK 177
                                                                                                                                                                                                                                                 ------PLRFGRNVQEERSAGATANLPLRSGRNMEVSLVRRVPNLPQRFGRTTTA 137
                                                                                                                                                                                                                                                                GAFPEIHIVQYPLDMGRKGKSKSSNSNTSNM---NGGGTTTSIV-----PVSVDSTGRV 122
                                                                                                                                                                                                                                                                                                  138 KSVCRMLSDLCQGSMHSPCANDLFYSMTCQHQEIQNPDQKQSRRLL-----FKKIDDAE 191
                                                                                                                                                                          Gaps
                                                                                                                                                                                                 34 NLHSKENYDKYSEPRGYPKGER--SLNFEELKDWGPKNVIKMSTPAVNKMPHSFANL--- 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-99187606; PubMed-9528757;
Kressler D., de la Cruz J., Rojo M., Linder P.;
"Dbp6p is an essential putative ATP-dependent RNA helicase required
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    for 60s-ribosomal-subunit assembly in Saccharomyces cerevisiae.";
Mol. Cell. Biol. 18:1855-1865(1989).
-i- FUNCTION: ATP-BINDING RNA HELICASE INVOLVED IN THE BIOGENESIS OF
60s RIBOSOMAL SUBUNITS AND IS REQUIRED FOR THE NORMAL FORMATION
                                                                                                                                                                                                                          13 NVYSNEEEDPLFQPKPKPRQQQKQQQQQGELND-KPKKVIPTYGNRKGYLPKNIEDFGDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                         37;
                                                                                                                                                Length 685;
                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SIMILARITY: BELONGS TO THE DEAD BOX HELICASE FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                             SH2-LIKE DOMAIN.
1DC8521E9997A583 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-OCT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
ATP-dependent RNA helicase DBP6 (DEAD-box protein 6)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Saccharomycetales; Saccharomycetaceae; Saccharomyces
                                                                                                                                                                          75;
                                                                                                                                               Score 84.5; DB 1;
Pred. No. 1.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBUNIT: Interacts with DBP9.
SUBCELLULAR LOCATION: Nuclear; nucleolar.
                                                                                                                                                                                                                                                                                                                                                                                                                                       629 AA.
                                                                                                                                                                          29; Mismatches
                                                               POLY-GLN.
                                                                                     PRO-RICH
                                                                                                   POLY-ASP
                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequ
            EMBL; U43887; AAB40497.1; -.
DictyDD; DD000074; SNWA.
InterPro; IPR004015; SKIP_SNW.
Pfam; PF02731; SKIP_SNW; 1.
                                                                                                                          78529 MW;
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                                                                                                                                                   8.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OF 25S AND 5.8S RRNAS
                                                                                                                                                                            44; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DBP6 OR YNR038W OR N3302
                                                                                      245
409
539
685 AA;
                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID-4932;
                                                                                                                                                                                                                                                                                                                                                    192 LKQEK 196
                                                                                                                                                                                                                                                                                                                                                                          178 IKSSK 182
                                                                                                                                                                                                                                                                                                                                                                                                                                        DBP6_YEAST
P53734;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pohl T.M.;
                                                                                                                           SEQUENCE
                                                                                                                                                   Query Match
                                                                DOMAIN
                                                                            DOMAIN
                                                                                                   DOMAIN
                                                                                                                DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          342 EADRILN-QSFQGWCPKLMSHLKTDKLDTLP-----GNVIKMIFSATLTTNTEKL 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     112 SGRNM------EVSLVRRVPNLPQRFG-RTTTAKSVCR---MLSDLCQGSMHSPCAND 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       52 KGERSLNPEELKDWGPKNVIKMSTPAVNKMPHSFANLPLRFGRNVQEERSAGATANLPLR 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        44; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. MEDLINE-88142836; PubMed-3325825; Marshall M., Mahoney D., Rose A., Hicks J.B., Broach J.R.; Marshall M., Mahoney D., Rose A., Hicks J.B., Broach J.R.; Functional domains of State a gene required for position effect regulation in Saccharomyces cerevisiae."; Mol. Cell. Biol. 7:4441-4452(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyceta
                                                                                                                                                                                                              PROSITE: PS00039; DEAD_ATP_HELICASE; 1.
Hydrolase; Helicase; ATP-binding; RNA-binding; Nuclear protein;
rNA processing; Ribosome biogenesis.
NP_BIND 234 241 ATP (POTENTIAL).
SITE 311 344 DEAD BOX.
SCOUGNCE 629 AA; 70361 MW; 64A04A2D88F44072 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Regulatory protein SIR4 (Silent information regulator SIR4 or STE9 OR ASD1 OR UTH2 OR YDR227W OR YD9934.12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABOUENCE FROM N.A. MEDLINE-95192063; PubMed=7885847; MEDLINE-95192063; PubMed=7885847; Davies C.J., Hutchison C.A. III; Davies C.J., Hutchison G.A. III; MINSERTION Site Specificity of the transposon Tn3."; Nucleic Acids Res. 23:507-514(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        51;
                                                                                                                                                                                                                                                                                                                                                                                                                 8.3%; Score 84; DB 1;
21.7%; Pred. No. 1.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    160 LEYSMTCQHQEIQNPDQKQSRRLLFKKIDDAELKQEK 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-0CT-1989 (Rel. 12, Created)
01-0CT-1989 (Rel. 12, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBUNIT: INTERACTS WITH RAP1 C-TERMINUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT; 1358 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 21.7%; Pred. No. 1.7; es 34; Conservative 28; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Saccharomyces cerevisiae (Baker's yeast).
                                                 InterPro; IPR000629; DEAD_box.
InterPro; IPR001650; Helicase_C.
                                                                                                        Pfam; PF00270; DEAD; 1.
Pfam; PF00271; helicase_C; 1.
SWART; SW00487; DEXDC; 1.
SWART; SW00490; HELICC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                          InterPro; IPR001410;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AND TELOMERES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=4932;
S0005321;
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P11978;
                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIR4_YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        391
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 940 K-----LSTTPTKSNRRVSHSDTNSSK--PKNTKENLSKSSWRQEWLANLKL-----IS 986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63 KDWGPKNVIKMSTPAVNKMPHSFANLPLRFGRNVQEERSAGA-----TANLPLRSGRNME 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        118 VSLVRRVPNLPQRFGRTTTAKSVCRMLSDLCQGSMHSPCANDL------FYSM 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        41; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDDINE-21848401; PubMed-11859360;
Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7 KLFILLTLATSSLLTSNIFCADELVMSNL----HSKENYDKYSEPRGYPKGERSLNFEEL 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DPOD_SCHPO STANDARD; PRT; 1086.AA.
P30316; Q10016; Q9USU0;
01-APR-1993 (Rel. 25, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-UNN-2002 (Rel. 41, Last annotation update)
DNA polymerase delta catalytic subunit (EC 2.7.7.7) (DNA polymerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pignede G., Bouvier D., de Recondo A.M., Baldacci G.; "Characterization of the POL3 gene product from Schizosaccharomyces pombe indicates inter species conservation of the catalytic subunit of DNA polymerase delta.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Park H., Francesconi S., Wang T.S.F.;
                                                                                                                                                                                                                                                                                       SGD; SO002635; SIR4.
Transcription regulation; Repressor; DNA-binding; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8.0%; Score 81.5; DB 1; Length 1358;
23.2%; Pred. No. 8.1;
lve 34; Mismatches 84; Indels 41;
                                                                                                                                                                                                                                                                                                                                                                                                                    994 994 P -> L.
1358 AA; 152061 MW; 9C698765964F094E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                      COILED COIL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         delta from Schizosaccharomyces pombe.";
Mol. Biol. Cell 4:145-157(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       165 TCQ----HQEIQN-PDQKQSRRLLFKK 186
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MEDLINE-92071954; Pubmed-1960723;
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Mol. Biol. 222:209-218(1991).
                                                                                                                                                    EMBL; M37249; AAA20881.1; -. EMBL; U13239; AAC33144.1; -. EMBL; Z48612; CAA88507.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23.2%;
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Best Local Similarity 23.2%;
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NCBI_TaxID=4896;
                                                                                                                                                                                                                                                         PIR; A29360; A29360.
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DPOD_SCHPO
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Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A., RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A., RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G., RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J., RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J., RA James K., Jones L., Murphy L., Niblett D., Odell C., RA Monory P., Moule S., McLean J., Saunders D., Seeger K., Sharp S., Skelton J., Simmonds M., Squares S., Stevens K., Skelton J., Simmonds M., Squares R., Squares S., Stevens K., Skelton J., Simmonds M., Squares R., Scheer R., Whitehead S., Ry Woodward J., Volckeart G., Aert R., Robben J., Grymonprez B., Weltjens I., Volckeart G., Aert R., Robben J., Grymonprez B., Weltjens I., Volckeart G., Aert R., Robben J., Grymonprez B., RA Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H., Reinhardt R., Pohl T.M., R. Gallbert R., Purnelle B., Grifeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S., R. Galbert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M., Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L., R. Acht R., Curzado L., Jimenez J., Sanchez M., Gallard B., R., Cruzado L., Jimenez J., Sanchez M., Gals R., Pohl S., R. Cerrutti L., Lowe T., McCombie W.R., Pulser P., Shpakovski G.V., Ussery D., Barrell B., R., Nurse P.; R. Nather A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L., R. Nather HJS; R.J. 1880 (20202).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -i- FUNCTION: THIS POLYMERASE POSSESSES TWO ENZYMATIC ACTIVITIES:
DNA SYNTHESIS (POLYMERASE) AND AN EXONUCLEOLYTIC ACTIVITY THAT
DEGRADES SINGLE STRANDED DNA IN THE 3' TO 5' DIRECTION.
-i- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate - N diphosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBDNIT: HETEROTETRAMER THAT CONSIST OF THE POL3, CDC1, CDC27 AND CDM1 SUBUNITS. THE POL3 SUBUNIT CONTAINS THE POLYMERASE ACTIVE SITE AND MOST LIKELY THE ACTIVE SITE FOR THE 3'-5' EXONUCLEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBCELLULAR LOCATION: Nuclear.
MISCELLANEOUS: IN EUKARYOTES THERE ARE FIVE DNA POLYMERASES:
ALPHA, BETA, GAMMA, DELTA, AND EPSILON WHICH ARE RESPONSIBLE FOR
DIFFERENT REACTIONS OF DNA SYNTHESIS.
SIMILARITY: BELONGS TO THE DNA POLYMERASE TYPE-B FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00116; DNA_POLYMERASE_B; 1.

Transferase; DNA-directed DNA polymerase; DNA replication;

DNA-binding; Hydrolase; Exonuclease; Zinc-finger; Nuclear protein.

ZN_FING 993 1011 C4-TYPE (POTENTIAL).

ZN_FING 1040 1058 C4-TYPE (POTENTIAL).
Chillingworth T., Churcher C.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KLEFEKVY -> NWSFST (IN REF. 1).
L -> H (IN REF. 1).
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8.6;
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T -> S (IN REF. 1).
R -> C (IN REF. 1 AND 2)
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00136; DNA_pol_B; 1.
Pfam; PF03104; DNA_pol_B_exo; 1.
PRINTS; PR00106; DNAPOLB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                123568 MW;
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EMBL; AL121815; CAB58156.1; -.
PIR; S19661; S19661.
InterPro; IPR002064; DNA_POl_B.
InterPro; IPR004578; Pol2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  102
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   Brooks K., Brown D.,
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           SOLUTION DE LA PRESENTA DEL PRESENTA DEL PRESENTA DE LA PRESENTA D
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Gaps

42;

36; Indels

20; Mismatches

Best Local Similarity 27.9 Matches 38; Conservative

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01-NOV-1997 (Rel. 35, Last annotation update)
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SEQUENCE
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YL01_YEAST
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                           249 DDLIL-----EHNYD-VSDPRNIFAQAARGPIAIIMDECMENLGGHKGVSKFFHAFPSK 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        77 AVNKMPHSFANLPLRFGRNVQEERS-AGATANLPLRSGRNMEVSLVRRVPNLPQRFGRTT 135
                                                                     1021 RQVAQVNDLEVRFARLWTQ----CQRSWHQDVICTSRDCPIFYMRIAEHKKLQ-1072
            IKMSTPAVNKMPHSFANLPLRFGRNVQEERSAGATANLPLRSGR-----NMEVSLVR 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DELVMSNLHSKENYDKYSEPRGY-----PKGERSLNFEELKD--WGPKNVIK----MSTP 76
                                                                                                                                                                                                                                                                                                                MEDILINE—83056843; PubMed-7142161; Gingeras T.R., Sciaky D., Gelinas R.E., Bing-Dong J., Yen C.E., Kelly M.M., Bullock P.A., Parsons B.L., O'Neill K.E., Roberts R.J.; Funcleotide sequences from the adenovirus-2, genome."; J. Biol. Chem. 257:13475-13491(1982).
                                                                                                                                                                                                                                                              Human adenovirus type 2.
Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
                                                         R----VPNLPQRFGRTTTAKSVCRMLSDLCQGSMHSP--CAN---DLFYSMTCQHQEIQN
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COLEF76D2E5012DC CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1;
                                                                                                                                                                                                                             Last annotation update)
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(Rel. 01, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7.8%; Score 79.5; D 25.0%; Pred. No. 3.1; Live 27; Mismatches
                                                                                                                                                                                  449 AA
                                                                                                                                                                                                                   Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                      or send an email to license@isb-sib.ch)
                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                       Maturation protein (Protein IVA2). PIVA2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR003389; Adeno_IVa2.
Pfam; PF02456; Adeno_IVa2; 1.
ATP-binding.
                                                                                                                                                                                                       21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last seq
01-NOV-1997 (Rel. 35, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    178 A
50881 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; J01917; AAA92205.1; -.
                                                                                                                    1073 ----QSVDLL-KRFDE 1083
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                                                                                                       174 PDQKQSRRLLFKKIDD 189
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449 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                          Viruses; dsDNA vi
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P03271;
21-JUL-1986 (
21-JUL-1986 (
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Local S...
40;
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SEQUENCE
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this SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        249 DDLIL----EHNYD-VSDPRNIFAQAAARGPIAIIMDECMENLGGHKGVSKFFHAFPSK 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28 DELVMSNLHSKENYDKYSEPRGY-----PKGERSLNFEELKD--WGPKNVIK----MSTP 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDILINE=92087470; PubMed=1727603; Chroboczek J., Bieber F., Jacrot B.; The sequence of the genome of adenovirus type 5 and its comparison with the genome of adenovirus type 2."; Virology 186:280-285(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                              'n
                                                                                                          Human adenovirus type 5.
Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
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Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                              MEDLINE-82211779; PubMed=7343420; wan Ormondt H.; van Beveren C.P., Maat J., Dekker B.M.M., van Ormondt H.; and beveren C.P., maat J., Dekker B.M.M., van Ormondt H.; leader segment of the major late mRNAs of adenovirus type 5."; Gene 16:179-189(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ou-wov-199/ (Rel. 35, Last sequence update)
Hypothetical 69.8 kba protein in BDF1-SFP1 intergenic region.
YERQUIC OR L8084.19.
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STRAIN=S288c / AB972;
Johnston M., Andrews S., Brinkman R., Cooper J., Ding H.,
Favello A., Fulton L., Gattung S., Greco T., Kirsten J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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20AD30752DCA96C2 CRC64;
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25.0%; Pred. No. 3.1;
Live 27; Mismatches 70;
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Maturation protein (Protein IVA2).
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Pfam; PF02456; Adeno_IVa2; 1.
ATP-binding.
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50887 MW;
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Best Local Similarity 25.0%;
"Arches 40; Conservative
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[2]
SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Engler J.A., van Bree M.P.;
The nucleotide sequence of the gene encoding protein IVa2 in human
adenovirus type 7.";
Gene 19:71-80(1982).
                                                                                                                                                                                                                       Lygerou Z., Conesa C., Lesage P., Swanson R.N., Ruet A., Carlson M., Sentenac A., Seraphin B.; Sentenac A., Seraphin B.; Sentenac A., Seraphin B.; The yeast BDF1 gene encodes a transcription factor involved in the expression of a broad class of genes including snRNAs."; Nucleic Acids Res. 22:5332-5340(1994).
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Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus
  Kucaba T., Hallsworth K., Hawkins J., Hillier L., Jier M., Johnson D., Johnston L., Langston Y., Latreille P., Le T., Mardis E., Menezes S., Miller N., Nhan M., Pauley A., Peluso D., Rifken L., Riles L., Taich A., Trevaskis E., Vignati D., Wilcox L., Wohldman P., Vaudin M., Wilson R., Waterston R.; Submitted (JAN-1995) to the EMBL/GenBank/DDBJ databases.
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609 AA; 69817 MW; 94B239C5B0F75909 CRC64;
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21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Maturation protein (Protein IVA2).
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InterPro; IPR001269; UPF0034.
InterPro; IPR000571; Znf_CCCH.
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Pfam; PF01207; UPF0034; 1
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ses 35; Conserv
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                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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6
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NCBI_TaxID=28284;
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van Ormondt H.;
Submitted (JUN-1985) to the EMBL/GenBank/DDBJ databases.
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K -> R (IN REF. 2).
01F17E29320848BC CRC64;
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01-FEB-1996 (Rel. 33, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
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MEDLINE-94087748; PubMed-8263936;
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Pfam; PF02456; Adeno_IVa2; 1.
ATP-binding.
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Pfam; PF02456; Adeno_IVa2; 1.
ATP-binding.
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                                                                                                                                                                                                                                                                                                                                                                                                       PIR; A03843; Q4ADA7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       448 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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SEQUENCE
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MCAK_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-98382520; PubMed-9714826; Wassem A., Alam Y., Dogan B., White K.N., Leigh I.M., Wassem N.H.; Wassen A., sequence and expression of the gene encoding human keratin
                                                                                      77 AVNKMPHSFANLPLREGRNVQEERSAGAT-ANLPLRSGRNMEVSLVRRVPNLPQRFGRTT 135
                                                                                                                                            302 LHDKFPKCTGYTVLVVLHNMNPRRDLGGNIANLKIQA--KMHLISPRMHPSQLNRFVNTF 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kuruc N., Leube R.E., Moll I., Bader B.L., Franke W.W.; "Synthesis of cytokeratin 13, a component characteristic of internal stratified epithelia, is not induced in human epidermal tumors."; Differentiation 42:111-123(1989).
                                                 Gaps
                                                                      28 DELVMSNLHSKENYDKYSEP----RGYPKGERSLNFEELKD--WGPKNVIK----MSTP 76
                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. MEDIANG-2477803; MEDIANE-9016882; PubMed-2477803; Mischke D., Schulz P., Wild A.G.; "The N., but not the C-terminal domains of human keratins 13 and 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VAKIANT WSN PRO-119.

WEDLINE-506083598; PubMed-7493031;

Richard G., de Laurenzi V., Didona B., Bale S.J., Compton J.G.;

"Keratin 13 point mutation underlies the hereditary mucosal

"Keratin 13 point mutation enderlies the hereditary mucosal

Petithelial disorder white sponge nevus.";

Nat. Genet. 11:453-455(1995).

-i - SUBGUNIT: HETEROTETRAMER OF TWO TYPE I AND TWO TYPE II KERATINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REVISION, SEQUENCE FROM N.A. MEDITE=89350978; Pubmed=2475110; Schulz P., Wachter E., Hochstrasser K., Wild A.G., Mischke D.; "Sequence of a human keratin 13 specific cDNA encompassing coil 1B through the 3' end.";
                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                         15-DEC-1998 (Rel. 37, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Keratin, type I cytoskeletal 13 (Cytokeratin 13) (K13) (CK 13).
                        Length 446;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Strausberg R.; Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
  51122 MW; C0969E192524A36E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Blochem. Biophys. Res. Commun. 162:1522-1527(1989).
                                                                                                                                                                    T---AKSVCRMLSDLCQGSMHSPCANDLFYSMTCQHQEIQ 172
                                                                                                                                                                                  360 TKGLPLAISLLLKDIFQFHAQKPCYDWIIYNTTPEHDALQ 399
                         DB 1;
                                                                                                                                                                                                                                                       458 AA
                                                26; Mismatches
                         Score 76.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     are closely related.";
Nucleic Acids Res. 17:7984-7984(1989).
                                      Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. MEDLINE-90228645; PubMed-2483837;
                                                                                                                                                                                                                                                                             01-JAN-1990 (Rel. 13, Created)
                          7.5%;
                                    24.48;
                                                 Conservative
                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gene 215:269-279(1998).
                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
   446 AA;
                                      Best Local Similarity
Matches 39; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-Pancreas;
                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9606;
                                                                                                                                                                                                                                                        K1CM_HUMAN
   SEQUENCE
                           Query Match
                                                                                                                                                                                                                                             K1CM_HUMAN
                                                                                                                                                                      136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /FTIG-VAR_003836.
G -> D (IN REF. 1 AND 2).
MIGFPSSAGSVSPRSTSVTTTSSASVTTTSNASGRRTSDVR
                                              USEASE: Detects in Anily and dominant disorder which predominantly affects noncornified stratified squamous epithelia. Clinically, it is characterized by the presence of soft, white, and spongy plaques in the oral mucosa. The characteristic histopathologic features are epithelial thickening, parakeratosis, and vacuolization of the suprabasal layer of oral epithelial keratinocytes. Less frequently the mucous membranes of the nose, esophagus, genitalia and rectum are involved.

MISCELLANEOUS: THERE ARE TWO TYPES OF CYPOSKELETAL AND MICROFLERILLAR KERATIN: I (ACIDIC, 40-55 kDa) [K9 TO K20] AND IT (NEUTRAL TO BASIC; 56-70 kDa) [K1 TO K8].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     :| : : | : : | 332
273 VLAEWREQYEAMAERNRRDAEEWFHAKSAELNKEVSTNTAMIQTSKTEITELRRTLQGLE 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---KMPHSFANLPLRFGRNVQE-----ERSAGATANLPLRSGRNMEVSLVRRV---- 124
                             DISEASE: Defects in KRT13 are a cause of white sponge nevus (WSN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28 DELVMSNLHSKENYDKYSEPRGYPKGERSLNFEELKDW-----GPKNVIKMSTPAVN--- 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----PNLPQRFG-RTTTAKSVCRMLSDL--CQGSMHSPCA--NDLFYSMTCQHQE 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    coil; Keratin; Disease mutation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 458;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R -> KRQP (IN REF. 3 AND 4).
9E033A247CD2B106 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
KERATIN 13 IS GENERALLY ASSOCIATED WITH KERATIN 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LINKER 12.
COIL 2.
L -> P (IN WSN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7.5%; Score 76.5;
23.4%; Pred. No. 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LINKER 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COIL 1A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COIL 1B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001664; IF.
InterPro; IPR002957; Keratin_I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ..., FrU0038; filament; 1.
PRINTS; PR01248; TYPELERATIN.
PROSITE; PS00226; IF; 1.
Intermediate filament. ...,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       458 AA; 49586 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; X14640; CAA32786.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AF049259; AAC35754.1;
EMBL; BC002661; AAH02661.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GlycoSuiteDB; P13646; -. Genew; HGNC:6415; KRT13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; X52426; CAA36673.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIR; S06088; KRHU3.
PIR; A33403; A33403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MIM; 193900;
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-!- FUNCTION: CATALYZES THE 14-ALPHA DEMETHYLATION OF OBTUSIFOLIOL TO 4 ALPHA-METHYL-5 ALPHA-ERGOSTA-8,14,24(28)-TRIEN-3 BETA-OL-
-!- CATALYZIC ACTIVITY: Obtusifoliol + 3 O(2) + 3 NADPH + 3 H(+) = 4-
alpha-methyl-5-alpha-ergosta-8,14,24(28)-trien-3-beta-ol + förmate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
Panicoideae; Andropogoneae; Sorghum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam: PF00067; p450; 1.
PROSITE; PS00086; CYTOCHROME_P450; 1.
Methyltransferase; Oxidoreductase; Monooxygenase; Electron transport;
                                                                                                                  DOVAAINPE------LLQLLPLHPKDNLPLQENVIIQKQKRRSVNSKIPAPKESLRSK 110
                                                                EELKDWGPKNVIKMSTPAVNKMP-HSFANLPLRFGRNVQEERSAGATANLPL-----R 111
                                                                                                                                                                                         111 STRMSTVSELRITAQENDMEVELPAAANSRKQFSVPPAPTRPSCPAVAEIPLRMVSEEME 170
1 MAMDSSLQARLFPGLAIKIQRSNGLIHSANVRTVNLEKSCVSVEWAE-GGATKG-KEIDF 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-JUN-2002 (Rel. 41, Last anotation update)
15-JUN-2002 (Rel. 41, Last anotation update)
15-JUN-2005 (Rel. 41, Last 13.70) (CYPL) (P450-LIA1) (Obtusifoliol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bak S., Kahn R.A., Olsen C.E., Halkier B.A.;
"Cloning and expression in Escherichia coli of the obtusifoliol 14
alpha-demethylase of Sorghum bicolor (L.) Moench, a cytochrome P450
orthologous to the sterol 14 alpha-demethylases (CYP51) from fungi
                                                                                                                                                                                                                                                                                                                                                                  GSMH----SPCANDL--FYSMTCQHQEIQNPDQKQSRRLLFKKIDDAELKQEK 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           + 3 NADP(+) + 3 H(2)0.
--- COFACTOR: Heme-thlolate.
--- PATHMAX: Sterol biosynthesis.
--- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              h 7.3%; Score 74.5; DB 1; Similarity 33.3%; Pred. No. 11; 18; Conservative 13; Mismatches 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-CV. SS1000; TISSUE-Etiolated seedling; MEDLINE-97231675; PubMed-9076987; Bak S., Kahn R.A., Olsen C.E., Halkier B.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sorghum bicolor (Sorghum) (Sorghum vulgare).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     492 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR001128; Cytochrome_P450.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; U74319; AAC49659.1; -. HSSP; P77901; 1E9X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14-alpha demethylase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Membrane; Heme; NADP
BINDING 434 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=4558;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CP51_SORBI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P93846;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Loca
Matches
                                                                   9
                                                                                                                                                                                                112
                                                                                                                                                                                                                                                                                                                          150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HEAD DRAWER WAS A PROCESS OF THE PRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mitted (CCT-2001) to the EMBL/GenBank/DDBJ databases.
FUNCTION: PRESENT THROUGHOUT THE CELL CYCLE, ASSOCIATES WITH CENTROWERS AT EARLY PROPHASE, AND REMAINS ASSOCIATED WITH THE CENTROMERES AT EARLY PROPHASE, BND REMAINS ASSOCIATED WITH THE CENTROMERE UNTIL AFTER TELOPHASE (BY SIMILARITY).
TISSUE SPECIFICITY: EXPRESSED AT HIGH LEVELS IN THYMUS AND TESTIS, AT LOW LEVELS IN SMALL INTESTINE, THE MUCOSAL LINING OF COLON, AND PLACENTA, AND AT VERY LOW LEVELS IN SPLEEN AND OVARY; EXPRESSION IS NOT DETECTED IN PROSTATE, PERIPHERAL'BLOOD LEUKOCYTES, HEART, BRAIN, LUNG, LIVER, SKELETAL MUSCLE, KIDNEY, OR PANCKEAS.
SIMILARITY: BELONGS TO THE KINESIN-LIKE PROTEIN FAMILY. MCAK/KIF2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kim I.-G., Jun D.Y., Sohn U., Kim Y.H.; "Cloning and expression of human mitotic centromere-associated kinesin
                           099661, 096C18; 096HB8; 16-CT-2001 (Rel. 40, Created) 15-JUN-2002 (Rel. 41, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Mitotic centromere-associated kinesin (MCAK) (Kinesin-like protein 6).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14 LATSSLLTSNIF--CADELVMSN--LHSKE----NYDK----YSEPRGYPKGERSLNF
                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KINESIN-MOTOR (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -> L (IN REF. 1).
-> P (IN REF. 2; AAH08764).
5BDECC133AB4B55C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7.4%; Score 75; DB 1; Length 725; 21.0%; Pred. No. 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     77; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS0041; KINESIN_MOTOR_DOMAIN1; 1.
PROSITE; PS50067; KINESIN_MOTOR_DOMAIN2; 1.
Motor protein; Microtubules; ATP-binding; Coiled coil;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COILED COIL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GLOBULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COILED COIL (PO ATP (POTENTIAL)
   725 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  43; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3iochim. Biophys. Acta 1359:181-186(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001752; kinesin_motor.
Pfam; PF00225; kinesin; 1.
SWART; SM00129; KISc; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-98094213; PubMed-9434124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BC014924; AAH14924.1; -. BC008764; AAH08764.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     81312 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; U63743; AAC27660.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
TISSUE-Kidney, and Uterus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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658
725
355
418
449
698
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415
449
698
725 AA;
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EMBL; BC008764; AAH(
HSSP; P17119; 3KAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       <del>..</del>
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                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nuclear protein
                                                                                                                                                                                                                                                                                                                                                                                                                               cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Strausberg R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MIM; 604538;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        49:
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DOMAIN
NP_BIND
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   STITITIE TO SOURCE TO SOUR
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Gaps
                                                                                                                                                67 PKNVIKMSTPA-VNKMPHSFANL----PLRFGRNVQEERSAGATANLPLRSGRN 115
                                                                                                   5;
492 AA; 55653 MW; 0C86160DFD812ECE CRC64;
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5

379 PKGHIVATSPSFANRLPHIYKNPDSYDPDRFGPGREEDKAAGAFSYISFGGRH 432

a

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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                            *Periodic charge distributions in the myosin rod amino acid sequence match cross-bridge spacings in muscle.";
Nature 299:226-231(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MISCELLANEOUS: MHC A AND MHC B ARE FOUND EXCLUSIVELY IN THE BODY
                                                                                                           Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MISCELLANEOUS: THERE ARE FOUR DIFFERENT MYOSIN HEAVY CHAINS IN
                                                                                                                                                                       MEDLINE-83273600; PubMed-6576334;
Rarn J., Brenner S., Barnett L.;
*Protein structural domains in the Caenorhabditis elegans unc-54
myosin heavy chain gene are not separated by introns.";
Proc. Natl. Acad. Sci. U.S.A. 80:4253-4257(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WALL MUSCLE. THEY CO-ASSEMBLE INTO BODY WALL THICK FILAMENT. SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOWAIN.
                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 1876-1966 FROM N.A.
MEDLINE-83232892; PubMed-6571695;
Wills N., Gesteland R.F., Karn J., Barnett L., Bolten S.,
Waterston R.H.;
                                                     Last sequence update)
                      1966 AA
                                                                                                                                                                                                                                                SEQUENCE OF 850-1966 FROM N.A. MEDLINE-82272395; PubMed-7202124; McLachlan A.D., Karn J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Myosin_tail
myosin_head.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Myosin_N.
                                              01, Created)
                                                        21-JUL-1986 (Rel. 01, Last se
16-OCT-2001 (Rel. 40, Last an
Myosin heavy chain B (MHC B).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; J01050; AAA28124.1; -. EMBL; V01494; CAA24738.1; -.
                      STANDARD;
                                                                                                      Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR004009;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (25)
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                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                           UNC-54 OR MYO-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A02992;
                                            21-JUL-1986
                       MYSB_CAEEL
RESULT 15
MYSB_CAEEL
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138 KSVCRMLSD----LCQGSMHSPCANDLF---YSMTCQHQEIQNPDQKQ-SRRLLFKKIDDA 190
                                                                                                                                                                                                                                                                                                                                                                                                                   59 FEELK------DWGPKNVIKMSTPAVNKMPHSFAN---LPLRFGRNVQEERSA---- 102
                                                                                                                                                                                                                                                                                                                                                                                                                                            582 MRHYAGTVRYNCLNWLEKNKDPLNDTVVSAMKQSKGNDLLVEIWQDYTTQEEAAAKAKEG 641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          642 GGGKKKGKSGSFWTVSMLYRESLNNLMTMLNKTHPHFIRCIIPNEKKQSGMIDAALVLN 701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                             1 MEIISSKLFILLTLATSSLL--TSNIFCADELVMSNLHSKENYDKYSEPRGYPKGERSLN 58
                                                                          protein; Coiled coil; Thick filament; Actin-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          103 GATANLPLRSGRNMEVSLVRR----------------VPNLPQRFGRTTTA----
                                                                                                                                                                                                                                                                                                                                     51;
                                                                                                                                                                                                                                                                                                           DB 1; Length 1966;
                                                                                                                                                                                                              METHYLATION (TRI-) (POTENTIAL).
ALKYLATION (SH-1).
ALKYLATION (SH-2).
E -> R (IN REF. 2).
I -> L (IN REF. 2).
                                                                                       Agr-binding; Methylation; Alkylation; Multigene family.

DOMAIN 851 1966 COILED COIL (POTENTIAL).

DOMAIN 851 1164 ALPHA-HELICAL TAILPIECE (S2)
                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                              B66F0BB2FE27B67F CRC64;
                                                                                                                                               HINGE.
LIGHT MEROMYOSIN (LMM).
                                                                                                                                                                                                                                                                                                                                     46; Mismatches 101;
                                                                                                                                                                       ATP (BY SIMILARITY)
ACTIN-BINDING.
ACTIN-BINDING.
                                                                                                                                                                                                                                                                                                                         Pred. No. 63;
                                                                                                                                                                                                                                                                                                            Score 74.5;
Pfam; PF00063; myosin_head; 1.
Pfam; PF01576; Myosin_tail; 1.
Pfam; PF02736; Myosin_N: 1.
PRINTS; PR00193; MYOSINHEAVY.
PRODOM; PD000355; myosin_head; 1.
SMART; SM00242; MYSC; 1.
                                                                                                                                                                                                                                                                                   225125 MW;
                                                                                                                                                                                                                                                                                                             7.38;
                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 19.2%;
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                                                                                                                                                                                                                                           715
1337
1880
                                                                                                                                                                                                                                                                                    1966 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     191 ELKQE 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               762 SLSEE 766
                                                                                 Myosin; Muscle
                                                                                                                                                                                                                                                                                                                                          47;
                                                                                                                                                                                                                                                                                     SEQUENCE
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Search completed: March 26, 2003, 10:14:30 Job time : 30 secs

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1 MEIISSKLFILLTLATSSLL........KQSRRLLFKKIDDAELKQEK 196
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1: /cgn2_6/ptodata/1/pubpaa/USOB_NEW_PUB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/CCT_NEW_PUB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/USO7_NEW_PUB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/USO7_NEW_PUB.pep:*

6: /cgn2_6/ptodata/1/pubpaa/USO7_NEW_PUB.pep:*

7: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*

8: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

9: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

9: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

10: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
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GenCore version 5.1.4_p5_4578
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          237916 seqs, 58723674 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                  OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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1018
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                                                                                                                                                                                                                                                                                                                                                                                                            Scoring table:
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                                                                                                                                                                                                                                                                                                Title:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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		Sequence 29, Appl	App	, Ap	,60	Appl	Appl	Appl	App	Appl	10504, 7	10, Appl	App	App	Appl	App	Appl	App	App	Appl
		29,	425,	425	140	33,	2,	7	20,		105	10	37,	45,	4	32	33,	39,	43,	47,
	ptio	uce	uce	ence	ence	nce	euce	ence	ence	euce	ence	ence	ence	ence	Sequence	Seguence	Sequence	ednence	Sequence	Sequence
	Description	edne	adne	Sequence 425, 1	Sequence 14009,	Sequence 33, Appl	Sequence 2,	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sedu	Sedu	Sedu	Segu	Sedu	Sedu
	De	Ň	Ñ			Ň														
		9	'n	25	US-09-815-242-14009		7		0	US-09-909-903-20	0504	0	7	'n		5	2	6	3	7
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 		5-79	4-13	38-5	115-2	97-9	117-4	35-6	196-1	5-601	115-2	140-7	-69	3-69	3-69	-69	-69	3-691	-691	-691
		JS-09-995-793A-29	JS-09-854-133-425	US-09-738-973-425	8-60	15-10-016-283-33	US-09-817-487A-2	US-10-135-687-2	US-09-796-138-20	5-60-	3-60	US-09-840-787-10	US-09-469-522-37	P-60.	JS-09-469-522-4	US-09-469-522-35	US-09-469-522-33	-60-	US-09-469-522-43	US-09-469-522-4
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ď	Query Match Length DB	9.66	8.1	8.1	8	7.4	7.4	7.3	7.2	7.2	7.2	7.1	7.1	7.1	7.1	7.1	7.1	7.1	7.1	7.1
	Score	1014	5.5	82.5	81	2.5	75.5	5.5	73	73	73	72.5	72	72	72	72	72	72	72	72
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	ult No.	-	7	m		'n	9	7	00	6	10	11	12	13	14	15	16	17	18	19
	Result No.																			

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31, P 25, P	Sequence 426, App Sequence 426, App Sequence 426, App
0. US-09-469-522-49 0. US-09-469-522-31 0. US-09-469-522-29 0. US-09-469-522-41 0. US-09-788-007-3 0. US-09-469-522-51 0. US-09-469-522-51 0. US-09-469-522-51 0. US-09-9738-626-4146 0. US-09-9738-626-4146 0. US-09-9738-628-4146 0. US-09-978-292-813-5 0. US-09-938-418-9 0. US-09-978-295A-459 0. US-09-978-192A-459 0. US-10-121-049-426 0. US-10-121-049-426	US-10-175-746-426 US-10-176-918-426 US-10-176-921-426
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## ALIGNMENTS

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GENERAL INFORMATION NO. US20030054446A1

Sequence 29, Application US/0995793A

Sequence 29, Application NO. US20030054446A1

PUBLICAID NO. US20030054446A1

GENERAL INFORMATION:

APPLICANT: Weber, Bernard H.F.

APPLICANT: Weber, Heidi

TILE OF INVENTION: NO. US20030054446A1e1 retina-specific human proteins C7orf

FILE REFERENCE: 033488-001

CURRENT APPLICATION NUMBER: US/09/995,793A

CURRENT APPLICATION NUMBER: 60/253,751

PRIOR FILING DATE: 2000-11-29

NUMBER OF SEQ ID NOS: 71

SOFTWARE: Patentin version 3.1

SEQ ID NO 29

LENGTH: 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 ELKDWGPKNVIKMSTPAVNKMPHSFANLPLRFGRNVQEERSAGATANLPLRSGRNMEVSL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 ELKDWGPRNVIKMSTPAVNKMPHSFANLPLRFGRNVQEERSAGATANLPLRSGRNMEVSL 120
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Pred. No. 7.8e-103;
1; Mismatches 0; Indels
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99.5%;
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Best Local Similarity 99.5
Matches 195; Conservative
                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Homo sapiens
US-09-995-793A-29
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65 WGPKNVIKMSTPAVNKMPH-----SFANLPLRFGRNVQE-----ERSAGATANLPLRS 112
                                                                                                   STPAVNKMPHSF-----ANLPLRFGRNVQEERSAGATANLPLRSGRNMEVSLVRRVPNL 127
         ---RGYPKGERSLNFEELKDWGPKNVIKM 73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT PRIOR DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-01-23
PRIOR FILING DATE: 2000-01-23
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
                                                                                                                                                                                                                             3834 PHTLNSTSTSKS----FQSTVTGELNAPYSKQFVHSKSSQYRKMK 3874
                                                                                                                                                                                              128 PQRFGRTTTAKSVCRMLSDLCQGSMHSPCANDLFYSMTCQHQEIQ 172
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SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Trawick, John D.
Carr, Grant J.
Yamamoto, Robert T.
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Zyskind, Judith W.
Wall, Daniel
              DELYMSNLHSKENYDKYSEP--
                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
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OTHER INFORMATION: Xaa
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US-10-016-283-33
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APPLICANT:
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                                                                                                        APPLICANT: LOGGES, Michael J.
APPLICANT: Mohamath, Raodoh
APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Robert A.
APPLICANT: Secrist, Heather
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: THE THERAPY AND DIAGNOSIS OF LUNG CANCER
TITLE REFERENCE: 210121.475c10
CURRENT PAPLICATION NUMBER: US/09/854,133
CURRENT FILING DATE: 2001-05-11
NUMBER OF SEQ ID NOS: 735
SOFTWARE: FastSEQ for Windows Version 3.0
LENGTH: 4019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 4019;
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APPLICANT: Mannion, Jane
APPLICANT: Kalos, Michael D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: THE THERAPY AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.47. ....
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8.1%; Score 82.5; DB 9;
20.6%; Pred. No. 21;
tive 27; Mismatches 61;
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20.6%; Pred. No. 21;
Live 27; Mismatches
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Secrist, Heather
Indirias, Carol Yoseph
Benson, Darin R.
Elliot, Mark
                                         Sequence 425, Application US/09854133
Publication No. US20020183499A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Henderson, Robert A.
Lodes, Michael J.
Fling, Steven P.
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Best Local Similarity 20.69
Matches 34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 20.6
Matches 34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Reed, Steven G.
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US-09-738-973-425
                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT; ORGANISM: Homo sapiens
US-09-854-133-425
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 3
US-09-738-973-425
RESULT 2
US-09-854-133-425
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ORGANISM: Triticum sp
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498 ISIMSSFAIFVLLTITT-----LYCCRRRKQWKNKKRESAAVTLTTLPSELLLDRLHP 550
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                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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Sequence 33, Application US/10016283
Fatent No. US20020164702A1
GENERAL INCPEMATION:
TITLE OF INVENTION: NOVEL TYROSINE KINASE RECEPTORS AND LIGANDS
FILE REFERENCE: REG195-B-PCT-US
CURRENT APPLICATION NUMBER: US/09/077,955A
PRIOR APPLICATION NUMBER: US/09/077,955A
PRIOR PILING DATE: 1998-09-10
PRIOR FILING DATE: 1998-09-10
PRIOR FILING DATE: 1998-12-13
PRIOR FILING DATE: 1996-12-13
SOFTWARE: PATENTIN NUMBER: PCT/US96/20696
SHOW FILING DATE: 1996-12-13
NUMBER OF SEQ ID NOS: 36
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                                                                                                                                                                                                                                                                                                                                                                                                                          69; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : | : : : | : : : | 656 EYMAYGDLNEFLRSMSPHTVCS--LSHSDLSMRAQVSSP 692
                                                                                                                                                                                                                                                                                                                                                                                        DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/09817487A
Fatent No. US20020150876A1
GENERAL INFORMATION:
APPLICATE: No. US20020150876A1artis AG
FILE REFERENCE: 4-31193A
CURRENT APPLICATION UNDBER: US/09/817,487A
CURRENT FILING DATE: 2002-02-14
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PATENTIN VETSION 3.0
                                                                                                                                                                                                                                                                                                                                                                                      Query Match 7.4%; Score 75.5; DB Best Local Similarity 20.1%; Pred. No. 14; Matches 44; Conservative 37; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Score 75.5; C; Pred. No. 14; 37; Mismatches
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nes 44; Conservative
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ORGANISM: homo sapiens
                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Homo sapiens US-10-016-283-33
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LENGTH: 869
                                                                                                                                                                                                                                                                           SEQ ID NO 33
LENGTH: 869
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Best Local S
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Sequence 20. Application US/09796138

patent No. US20020031782A1

patent No. US20020031782A1

general information: Michael R.

APPLICANT: Waterman, Michael R.

APPLICANT: Bellamine, Aouatef

APPLICANT: Bellamine, Aouatef

TITLE OF INVENTION: AND

TITLE OF INVENTION: AND

TITLE OF INVENTION: AND

TITLE OF INVENTION: AND

TITLE OF INVENTION: RELATING TO SAME

TITLE OF INVENTION: RELATING TO SAME

FILE REFERENCE: Attorney Docket No. US20020031782A1 1242-17-2

CURRENT FILING DATE: 2001-02-28

PRIOR APPLICATION NUMBER: 09/345,218

PRIOR PLILING DATE: 1999-06-30
                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: CHANDRAMOULISWARAN, IShwar et al.
TITLE OF INVENTION: ACID MOLECULES ENCOPING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
FILE REPERENCE: CLOOllo68DIV
CURRENT APPLICATION NUMBER: US/10/135,687
CURRENT APPLICATION NUMBER: US/10/135,687
PRIOR APPLICATION NUMBER: 09/749,588
PRIOR FILING DATE: 2000-12-28
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           83 HSFANLPLRFGRNVQEERSAGATANLPLRS------GRNMEVSLVRRVPNLPQR-- 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          335 VIDFGSASHVSKAVCSTYLQSRYYRAPEIILGLPFCEAIDMWSLGCVIAELFLGWPLYPG 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31 VMSNLHSKENYDKYSEPRGYP----KGERSLNFEELK----DWGPKNVIKMSTPAVNKMP 82
605 MVAVKM---LKEEASADMQADF-----QREAALMAEFDNPNIVKLLGVCAVGKPMCLLF 655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        237 ILSRL-SSENADEYNFVRSYECFOHKNHTCLVFEMLEONLYDFLKON------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Score 74.5; DB 12;
; Pred. No. 28;
33; Mismatches 53;
                                                        ---SMHSPCANDLFYSMTCOHQEIQNP 174
                                                                                          157 ANDLFYSMTCQHQEIQNP-DQKQSRRLLFKKIDD 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |:: | |: | |: |:395 ASE--YDQTPEEHELETGIKSKEARKYIFNCLDD 426
                                                                                                                                                                                                                                              Sequence 2, Application US/10135687
Patent No. US20020123120A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 7.3%;
Best Local Similarity 22.9%;
Matches 49; Conservative 3
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SEQ ID NO 20
LENGTH: 280
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Homo sapiens
US-10-135-687-2
                                                              145 SDLCQG-----
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US-09-796-138-20
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87 NLPLREGRNVQEERSA-----GATANLPLR----SGRNMEVSL------VRRVPNL 127
                                                                                                                                                                                                                                                                                                                                                                                                                                     36 HSKENYDKY-----SEPRGYPKGERSLNFEELKDWGPKNVIKMSTPAVNKMPHSFA 86
                                                                                                                                                                                                                                                                                                                                                   DB 10; Length 648;
18;
                                                                                                                                                                                                                                                                                                                                                                                                 48; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Yue, Henry
Guegler, Karl J.
Corley, Neil C.
TITLE OF INVENTION: HUMAN REGULATORY MOLECULES
NUMBER OF SEQUENCES: 98
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0356 US
PRIOR APPLICATION NUMBER: 60/242,5/8
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SEQ ID NO 10504
SEQ ID NO 10504
                                                                                                                                                                                                                                                                                                                                                   Query Match 7.2%; Score 73; DB Best Local Similarity 24.8%; Pred. No. 18; Matches 34; Conservative 21; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/840,787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 09/518,865
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Hillman, Jennifer L.
Bandman, Olga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 23-Apr-2001 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 10, Application US/09840787 Patent No. US20020058264A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Au-Young, Janice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                      GGANISM: Enterococcus faecalis US-09-815-242-10504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
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359 ALVGPNGIGKSTLLKSI 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Shah, Purvi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Palo Alto
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Sequence 20, Application US/0909903
Fatent No. US20020052031A1
GENERAL INRORANTION:
APPLICANT: Waterman, Michael R.
APPLICANT: Bellamine, Aouatef
TITLE OF INVENTION: WICLIEIC ACIDS AND THERAPEUTIC AND SCREENING METHODS
TITLE OF INVENTION: RELATING TO SAME
TITLE OF INVENTION: RELATING TO SAME
FILE REPERENCE: Atcorney Docket No. US20020052031A1 1242-17
CURRENT APPLICATION NUMBER: US/09/909,903
CURRENT FILING DATE: 2001-07-20
NUMBER OF SEQ ID NOS: 21
SOFTWARE: PATENTING VOICE: 21
SEQ ID NO 20
LENGTH: 280
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    56 SLNFEELKDWG-PKNVIKMSTPA-VNKMPHSFANL----PLRFGRNVQEERSAGATANLP 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             56 SLNFEELKDWG-PKNVIKMSTPA-VNKMPHSFANL----PLRFGRNVQEERSAGATANLP 109
                                                                                                                                                                    Length 280;
                                                  Length 280;
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                                                                                               25; Indels
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TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 10;
                                                      Score 73; DB 10;
Pred. No. 5.6;
                                                      Query Match 7.2%; Score 73; DB 10
Best Local Similarity 33.3%; Pred. No. 5.6;
Matches 22; Conservative 13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 7.2%; Score 73; DB 1
Best Local Similarity 33.3%; Pred. No. 5.6;
Matches 22; Conservative 13; Mismatches
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PRIOR PELLING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
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Patent No. US20020061569A1
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Carr, Grant J.
Yamamoto, Robert T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ohlsen, Kari L.
Zyskind, Judith W.
Wall, Daniel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Triticum sp. US-09-909-903-20
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                                                                                                                                                                                                                             110 LRSGRN 115
                                                                                                                                                                                                                                                                        215 FGGGRH 220
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                                                                                                                                                                                                                                                                                                                                          RESULT 9
US-09-909-903-20
           US-09-796-138-20
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
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387 SFIKAEGNLTREMIKHLERCEHRIMESLAWLSDSPLFDLIKQSKDREGPTDHLESACPL- 445
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NLHSKENYDKYSEPR 48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Benedict, William F.
Benedict, William F.
Zhou, Yunli
TITLE OF INVENTION: MODIFIED RETINOBLASTOMA TUMOR SUPPRESSOR
PROTEINS
                                                                                                                                                                                                                                                                                                                                           Length 781;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:

MEDIUM TYPE: FLORDY disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/469,522
FILING DATE: 22-Dec-1999
CLASSIFICATION: <unimal control of the company of
                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                   63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          149 QGSMHSPCANDLFYSMTCQHQEIQNPDQKQSRRLLFKKI 187
                                                                                                                                                                                                                                                                                                                                           Match 7.1%; Score 72; DB 10; Local Similarity 21.5%; Pred. No. 30; les 47; Conservative 23; Mismatches 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               UTXC:506
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                                                                                   TYPE: mino acid;
TYPE: mino acid
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 37:
US-09-469-522-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 09/026,459
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ATTORNEY/AGENT INPORMATION:
NAME: HIDLer, David W.
REGISTRATION NUMBER: 41,071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 45, Application US/09469522 Patent No. US20020151461A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 797 amino acids TYPE: amino acid
                                                                           LENGTH: 781 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17 SSLLTSNIF-----CADELVMS---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FELEFAX: 512/474-7577
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STREET: P.O. Box 4433
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SEQUENCE CHARACTERISTICS:
INFORMATION FOR SEQ ID NO: 37:
                             SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hu, Shi-Xue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Xu, Hong-Ji
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SECUENCES:
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ZIP: 77210-4433
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Matches
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6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             170 PASSMCLLAPCYLTGDSVRDKCVEMLSAALKADDDYKDYGVNCDKMASEIEDHIYQELKS 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           76 PAVNKMPHSFANLPLRFGRNVQEERSAGATANLPLRSGRNMEVSLVRRVPNLPQRFGRTT 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           112 -AGLSPPRKKREDPKTRRDSVDSKSSASSSPKRPSVERSNSSKSKAES-PKTPSSPLTPT 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           59 CSDKEVVSLAKVLIKNWKRLLDSPGPPKGEKGEEREKAKKKEKGLECSDWKPE----- 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26 CADELVMSNLHSK-ENYDKYSEPRGYPKGERSLNFEELK------DWGPKNVIKMST 75
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Zhou, Yunli
TITLE OF INVENTION: MODIFIED RETINOBLASTOMA TUMOR SUPPRESSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 348;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
COMPUTER: TBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/469,522
FILING DATE: 22-Dec-1999
CLASSIFICATION: <unimoderate the company of the company 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 10;
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NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: UTXC:506
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7.1%; Score 72.5; 22.2%; Pred. No. 8.
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. APPLICATION NUMBER: 09/026,459
. FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE DESCRIPTION: SEQ ID NO: 10 US-09-840-787-10
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US-09-469-522-37
Sequence 37, Application US/09469522
Fatent No. US20020151461A1
GENERAL INFORMATION:
APPLICANT: Xu, Hong-Ji
Hu, Shi-Xu
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROTEINS
                                                                                                                                                               LENGTH: 348 amino acids
TYPE: amino acid
STRANDEDNESS: single
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        TELEFAX: 415-845-4166
                                     TELEX: <UNKNOWN>
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: MUSCNOT01
CLONE: 118160
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Best Local Similarity 22.2%
watches 42; Conservative
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ZIP: 77210-4433
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122 SFIKAEGNLTREMIKHLERCEHRIMESLAWLSDSPLFDLIKOSKDREGPTDHLESACPL- 480
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                                                                   NLHSKENYDKYSEPR 48
                                                                                                                                           ---- DWGPKNVIKMSTPAVNKMPHSFANLPLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Xu, Hong-Ji
Hu, Shi-Xue
Benedict, William F.
Zhou, Yunii
TITLE OF INVENTION: MODIFIED RETINOBLASTOMA TUMOR SUPPRESSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 832;
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                                Indels
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SOFTWARE: Patentin Release #1.0, Version #1.30
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                                                                                                                                                                                                                                                                                            149 QGSMHSPCANDLFYSMTCQHQEIQNPDQKQSRRLLFKKI 187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ed. No. 33;
Mismatches
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ADDRESSEE: Arnold, White & Durkee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/469,522
FILING DATE: 22-Dec-1999
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         UTXC: 506
               ed. No. 32;
Mismatches
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MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 35:
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Pred. No. 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
                 Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 35, Application US/09469522 Patent No. US20020151461A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
21.5%; Pic. 23;
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Best Local Similarity 21:5%;
Matches 47; Conservative 2:
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                                                                                                                                               49 GYPKGERSLNFEELK-----
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                                    Conservative
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               Best Local Similarity
Matches 47; Conserv
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                                                                                                                                                                                        SFIKAEGNLTREMIKHLERCEHRIMESLAWLSDSPLFDLIKQSKDREGPTDHLESACPL-461
                                                                                                                                                                  -----NLHSKENYDKYSEPR 48
                                                                                                                                                                                                                                          DWGPKNVIKMSTPAVNKMPHSFANLPLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zhou, Yunli
TITLE OF INVENTION: MODIFIED RETINOBLASTOMA TUMOR SUPPRESSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 816;
                                                                                           Score 72; DB 10; Length 797;
                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                             63;
                                                                                                                                                                                                                                                                                                                                                                                                               149 QGSMHSPCANDLFYSMTCQHQEIQNPDQKQSRRLLFKKI 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: UTXC:506
TELECOMMUNICATION:
                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/09/469,522
FILING DATE: 22-Dec-1999
CLASSIFICATION: <Unknown>
           ; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 45:
US-09-469-522-45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 09/026,459
FILING DATE: <UNKNOWN>
ATTORNEY/AGENT INFORMATION:
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MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-469-522-4
                                                                                                              Pred. No
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Benedict, William F. Zhou, Yunli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                  17 SSLLTSNIF-----CADELVMS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4, Application US/09469522 Patent No. US20020151461A1 GENERAL INFORMATION:
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                                                                                                                             23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: P.O. Box 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS
                                                                                           ch 7.1%;
1 Similarity 21.5%;
47; Conservative 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Xu, Hong-Ji
Hu, Shi-Xue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Houston
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                                                                                                                                                                                                                                          49 GYPKGERSLNFEELK-
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                                                                                           Query Match
Best Local S
Matches 47
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86;

DB 10;

Score 72;

7.18;

Query Match

g	378	378 SKLLNDNIFHMSLLACALEVVMATYSRSTSQNLDSGTDLSFPWILNVLNLKAFDFYKVIE 437	137
٥٧	49	49 GYPKGERSLNFEELKDWGPKNVIKMSTPAVNKMPHSFANLPLR 91	
qa	438	OREGPT	961
οy	93	92 FGRNVQEERSAGATANLPLRSGRNMEVSLVRRVPNLPQRFGRTTTAKSVCRMLSDLC 148	148
Q	497		535
οy	149	149 QGSMHSPCANDLFYSMTCQHQEIQNPDQKQSRRLLFKKI 187	
đ	536	536ATSAFQTQKPLKSTSLSLFYKKV 558	
Sear	ch cor time	Search completed: March 26, 2003, 10:23:51 Job time : 20 secs	

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March 26, 2003, 10:08:29; Search time 35 Seconds (without alignments) 746.203 Million cell updates/sec
                                                                                                                                                                                                                                                                                                       US-09-831-758A-8
1018
1 MEIISSKLFILLTLATSSLL..........KQSRRLLFKKIDDAELKQEK 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /SIDS2/gcgdata/geneseq/yeneseqp-embl/AA1980.DAT:
/SIDS2/gcgdata/geneseq/yeneseqp-embl/AA1981.DAT:
/SIDS2/gcgdata/geneseq/yeneseqp-embl/AA1982.DAT:
/SIDS2/gcgdata/geneseqy/geneseqp-embl/AA1983.DAT:
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/SIDS2/gcgdata/geneseqy/geneseqp-embl/AA1988.DAT:
GenCore version 5.1.4\_p5\_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     908470 seqs, 133250620 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                     OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Perfect score:
Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

/SIDS2/gcgdata/geneseq//geneseqp-embl/AA1998.DAT./SIDS2/gcgdata/geneseq//geneseqp-embl/AA1999.DAT./SIDS2/gcgdata/geneseq//geneseqp-embl/AA2000.DAT./SIDS2/gcgdata/geneseq//geneseqp-embl/AA2000.DAT./SIDS2/gcgdata/genesen/mana.

/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1997

/SIDS2/gcgdata/geneseq/geneseqp-embl/AA2002.DAT

/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1993.DAT: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1994.DAT: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1995.DAT: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1996.DAT:

/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1989 /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1990 /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1992 /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1992

### SUMMARIES

Description	Novel human G-prot Amino acid sequenc Human retina speci Human retina speci Human G-prot Amino acid sequenc Novel bovine G-pro Amino acid sequenc Novel rat G-protei Amino acid sequenc	
aı	AAY93141 AAG67748 AAU99162 AAY93140 AAG67747 AAG67749 AAG67749 AAG67749	
DB	22 23 23 23 23 23 23 23 23 23 23 23 23 2	
å Duery Match Length DB	196 196 196 180 180 180 196 196 203	
% Ouery Match	100.0 100.0 100.0 92.3 92.3 66.2 66.2 54.3	
Score	1018 1018 1018 940 940 674 674 552.5	
Result No.	2 2 4 4 7 7 7 9 9	

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Fukusumi S;
                                                                     G-protein coupled receptor; human; bovine; nervous system disorder; rat; mouse; somatostatin excretion.
                                                                                                                                                                                                                                                            Watanabe T, Kikuchi K, Terao Y, Shintani Y, Hinuma S,
Fujii R, Hosoya M, Kitada C;
                                                      Novel human G-protein coupled receptor #2.
AAY93141 standard; Protein; 196 AA.
                                                                                                                                                                                     99JP-0060030.
99JP-0106812.
99JP-0166672.
                                                                                                                                                                                                                                          (TAKE ) TAKEDA CHEM IND LTD.
                                                                                                                                                           99WO-JP06283
                                                                                                                                                                                                                99JP-0221640
99JP-0259818
                                                                                                                                                                            98JP-0323759
                                     06-DEC-2000 (first entry)
                                                                                                                      WO200029441-A1.
                                                                                                     Homo sapiens
                                                                                                                                                                                                        14-JUN+1999;
04-AUG-1999;
14-SEP-1999;
                                                                                                                                                          11-NOV-1999;
                                                                                                                                       25-MAY-2000
                                                                                                                                                                             13-NOV-1998
                                                                                                                                                                                       08-MAR-1999
14-APR-1999
                    AAY93141;
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Weber BHF;
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                                                                                                                                                                                                               196;
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                                                                                                                                                                                            Query Match
                                                                                                                                                                                                        Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; prolactin secretion; hypoovarianism; sperm development; osteoporosis; lactation disorder; hypothyroidism; kidney failure; menopause; hyperprolactinemia; pitulitary tumour; diencephalon tumour; menstrual disorder; stress; autoimmune disease; prolactinoma; sterility; impotence; amenorrhea; lactorrhea; hyperpituitarism; Sheehan's syndrome Chairi-Frommel syndrome; spermatogenesis disorder.
                                                                                    receptor (GPCR) genes and their encoded proteins. This sequence represents the protein sequence of a human GPCR. The DNAs and proteins are used for the treatment, prevention and diagnosis of disorders of the nervous system. The proteins and its fragments are also promoters
                                                                                                                                                                                                                                                                                ELKDWGPKNVIKMSTPAVNKMPHSFANLPLRFGRNVQEERSAGATANLPLRSGRNMEVSL 120
                                                                                                                                                                                                                                                      G protein coupled receptor protein and antibodies to it for treatment and diagnosis of nerve diseases
                                                                                                                                                                                                                1 MEIISSKLFILLTLATSSLLTSNIFCADELVMSNLHSKENYDKYSEPRGYPKGERSLNFE 60
                                                                                                                                                                                     Gaps
                                                                                                                                                                                                       MEIISSKLFILLTLATSSLLTSNIFCADELVMSNLHSKENYDKYSEPRGYPKGERSLNFE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Amino acid sequence of a human prolactin secretion regulating agent.
                                                                           to the isolation of novel G-protein coupled
                                                                                                                                                                                    ö
                                                                                                                                                                21; Length 196;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matsumoto Y, Watanabe T, Hinuma S, Habata Y, Yoshida
                                                                                                                                                                                    Indels
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0
                                                                                                                                                              ; Score 1018; DB 2; Pred. No. 5e-106; 0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                         AAG67748 standard; Protein; 196 AA
                                                       Claim 2; Fig 3; 184pp; Japanese.
                                                                                                                                                               100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000JP-0378001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (TAKE ) TAKEDA CHEM IND LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                           of somatostatin excretion.
                                                                                                                                                                                                                                                                                                                                   RLLFKKIDDAELKQEK 196
                                                                                                                                                                        Best Local Similarity 100.
Matches 196; Conservative
                                                                           The invention relates
WPI; 2000-387747/33.
N-PSDB; AAA70501.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-596812/67
                                                                                                                                              196 AA;
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                                                                                                                                              Sequence
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Best Local S
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secretion regulating agent. The prolactin secretion regulating agent polypeptide and polynucleotide are used for the treatment and prevention of hypocovarianism, sperm under development, osteoporosis, menopause, lactation disorders, hypothyrodism, kidney failure, hyperprolactinemia, pituitary tumour, diencephalon tumour, menstrual disorders, stress, autoimnune disease, prolactinoma, sterility, impotence, amenorhea, lactorinea, hyperpituitarism, Chairi-Frommel syndrome, Argonz-del Castilo syndrome, Forbes-Albright syndrome, lyphoma, Sheehan's syndrome
                                                                                                                                                                             present sequence represents a human polypeptide which is a prolactin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VRRVPNLPQRFGRTTTAKSVCRMLSDLCQGSMHSPCANDLFYSMTCQHQEIQNPDQKQSR 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ELKDWGPKNVIKMSTPAVNKMPHSFANLPLRFGRNVQEERSAGATANLPLRSGRNMEVSL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MEIISSKLFILLTLATSSLLTSNIFCADELVMSNLHSKENYDKYSEPRGYPKGERSLNFE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New polypeptide, useful as a vasotropic, tranquilizing, immunosuppressive and gynecological agent comprises the prolactin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; MPP4; C7orf9; C12orf7; F379; retina specific gene;
AMD; age-related macular degeneration; blindness; gene therapy;
Ophthalmological; transgenic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 196;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human retina specific protein C7orf9 variant protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 1018; DB 22;
100.0%; Pred. No. 5e-106;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAU99162 standard; Protein; 196 AA.
                                                                                                                        Claim 2; Fig 3; 180pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (MULT-) MULTIGENE BIOTECH GMBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       and spermatogenesis disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29-NOV-2000; 2000US-253751P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HILLIHIHIHIHIH
RLLFKKIDDAELKQEK 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                               secretion regulator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 196 AA;
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Misc-difference
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Cl2orf7, MPP4 or F379, useful for diagnosing age-related macular degeneration or predisposition for macular degeneration, and in gene
                                                                              nucleic acids encoding retina-specific human protein Clorf9,
WPI; 2002-508512/54.
                                                                                  Novel
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Example 2; Page -; 120pp; English.

therapy techniques

controlly of the protein, the accusant underposition of activity of the accusant degeneration, comprising administering to a mammalian subject a reagent which decreases, inhibits or increases expression of Tooffy, MPD4 and/or F379 or which leads to the expression of a biologically active CTORF9, C120rf7, MPD4 and/or F379 protein and a transgenic non-human animal comprising at least one of the protein and a transgenic non-human animal comprising at least one of the nucleic acids (active or inactivated). The nucleic acid or protein is useful for diagnosing macular degeneration, preferably age-related macular degeneration (AMD) or a predisposition for macular degeneration. The the diagnosis is a CTORF9, where CTORF7, MPD4- or F379 repectfic nucleic acid probe, or anti-C70rf9, anti-C120rf7, anti-MPD4 or anti-F379-antibody. The reagent is detectably labeled, with a compound compound, a fluorescent compound, a chemiluminescent compound, a fluorescent compound, a metal chelate or an enzyme. Fragments of the nucleic acid are useful as probes or primers in a diagnostic assay, and for identifying further factors involved in development and conflare degeneration. The proteins encoded by the nucleic acid are useful are degeneration. The proteins which are accepted and are useful are degeneration. The proteins which are accepted and are useful as degeneration and for use in screening methods and are useful as decreased and servening methods. based on protein/protein interactions. The nucleic acid is also useful as reagents for detecting differences between normal and aberrant expression of the protein. the nucleic acid is also useful in gene therapy techniques, and can be used for gene targeting and/or gene replacement for restoring a mutant gene or for creating a mutant gene via homologous recombination. the protein can be used to identify other proteins involved in development and progression of macular degeneration. The present sequence represents a variant of the retina specific protein The invention relates to isolated nucleic acid encoding retina-specific minan protein C70xf9. Cl20xf7, MPP4 or F379 or a fragment, derivative or allelic variation of the above mentioned nucleic acid sequences. Also included are a recombinant vector containing the nucleic acid, a recombinant host cell which contains the vector and expresses the protein, an inhibitor characterised in that it can suppress the activity of the protein, treating macular degeneration or a 

Note: The present sequence is not shown in the specification but was created by the indexer using the sequence appearing as ABG66919 and the information in example 2.

196 AA; Sequence

ö Gaps 1 MEIISSKLFILLTLATSSLLTSNIFCADELVMSNLHSKENYDKYSEPRGYPKGERSLNFE 60 ö DB 23; Length 196; Indels 100.0%; Score 1018; DB 23; 100.0%; Pred. No. 5e-106; ive 0; Mismatches 0; Best Local Similarity 100. Matches 196; Conservative Query Match ò

- a
  - ELKDWGPKNVIKMSTPAVNKMPHSFANLPLRFGRNVQEERSAGATANLPLRSGRNMEVSL 120 61 ö
- 61 ELKDWGPKNVIKMSTPAVNKMPHSFANLPLRFGRNVQEERSAGATANLPLRSGRNMEVSL 120 a
- VRRVPNLPQRFGRTTTAKSVCRMLSDLCQGSMHSPCANDLFYSMTCQHQEIQNPDQKQSR 180 121 ò g
- RLLFKKIDDAELKQEK 196 181 ò
  - 181 a

RESULT 4 ABG66919

ABG66919 standard; Protein; 196 AA. GI

Human retina specific protein encoded by cDNA Clorf9 (first entry) 24-SEP-2002 ABG66919; 

Human; MPP4; C7orf9; C12orf7; F379; retina specific gene; AMD; age-related macular degeneration; blindness; gene therapy; Ophthalmological; transgenic.

Homo sapiens.

WO200244366-A2.

06-JUN-2002.

29-NOV-2001; 2001WO-EP13940.

29-NOV-2000; 2000US-253751P.

(MULT-) MULTIGENE BIOTECH GMBH.

Weber BHF; Stoehr HB,

WPI; 2002-508512/54. N-PSDB; ABK95399 Novel nucleic acids encoding retina-specific human protein C7orf9, C12orf7, MPP4 or F379, useful for diagnosing age-related macular degeneration or predisposition for macular degeneration, and in gene therapy techniques

Claim 1; Fig 9; 120pp; English.

The invention relates to isolated nucleic acid encoding retina-specific human protein C7orf9, C12orf7, MPP4 or F379 or a fragment, derivative or human protein C7orf9, C12orf7, MPP4 or F379 or a fragment, derivative or allelic variation of the above mentioned nucleic acid sequences.

Also included are a recombinant vector containing the nucleic acid, a recombinant host cell which contains the vector and expresses the crecombinant host cell which contains the vector and expresses the activity of the protein, treating macular degeneration or a predisposition for macular degeneration, comprising administering to a capturity of the protein, treating macular degeneration or a protein and a transgenic non-human animal comprising at least one of the corporation and a transgenic non-human animal comprising at least one of the nucleic acids (active or inactivated). The nucleic acid or protein is useful for diagnosing macular degeneration, for macular degeneration.

The reagent used in the diagnosis is a c7orf9, c12orf7, MPP4 or F379 continual degeneration (AMD) or a predisposition for macular degeneration.

The reagent used in the diagnosis as a c7orf9, c12orf7, mPP4 or F379 continual acid probe, or anti-C7orf9, anti-C12orf7, anti-MPP4 or compound, a fluorescent compound, a metal chelate or an enzyme. Fragments or the nucleic acid acid are useful as probes or primers in a diagnosit.

Confund as a radioisotope, a bioluminescent compound, a chemiluminescent compound, a coff the nucleic acid act useful as probes or primers in a diagnosit and easier useful as probes or primers in a diagnosit confund act useful as probes or primers in a diagnosit confund act useful as probes or primers in a diagnosit confund actual degeneration. The proteins which are useful as associated with macular degeneration and for use in screening methods associated with macular degenerations. The nucleic acid is also useful as a section the protein interactions. The nucleic acid are useful as a section the protein interactions also useful as a social of the protein. the nucleic acid is also useful in gene therapy techniques, and can be used for gene targeting and/or gene replacement for restoring a mutant gene or for creating a mutant gene via homologous recombination. the protein can be used to identify other proteins involved in development and progression of macular degeneration. The present sequence represents a retina specific protein of

196 AA; Sequence

Query Match

Score 1014; DB 23; Length 196; 99.68; 9

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MEIISSKLFILLTLATSSLLTSNIFCADELVMSNLHSKENYDKYSEPRGYPKGERSLNFE
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07-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-DEC-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                              AAG67747;
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                                                                                                                                                                     ELKDWGPKNVIKMSTPAVNKMPHSFANLPLRFGRNVQEERSAGATANLPLRSGRNMEVSL 120
                                                                                                                                                                                               61 ELKDWGPKNVIKMSTPAVNKMPHSFANLPLRFGRNVQEERSAGATANLPLRSGRNMEVSL 120
                                                                                                                                                                                                                                                                        VRRVPNLPQRFGRTTTAKSVCRMLSDLCQGSMHSPCANDLFYSMTCQHQEIQNPDQKQSR 180
                                                                                                                                                                                                                                                                                                  121 VRRVPNLPQRFGRTTTARSVCRMLSDLCQGSMHSPCANDLFYSMTCQHQEIQNPDQRQSR 180
                       Gaps
                                                                     Fukusumi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   G-protein coupled receptor; human; bovine; nervous system disorder;
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                       Indels
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Best Local Similarity 100.0%; Pred. No. 2.6e-97;
Matches 180; Conservative 0; Mismatches 0;
1.4e-105;
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                    Mismatches
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  Pred.
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soya M, Kitada C;
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99JP-0060030.
99JP-0106812.
99JP-0166672.
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RLLFKKIDDAELKQEK 196
                       Conservative
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N-PSDB; AAA70500.
Similarity
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                       195;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human: prolactin secretion; hypocvarianism; sperm development; osteoporosis; lactation disorder; hypothyroidism; kidney failure; hyperprolactinemia; pituitary tumour; diencephalon tumour; menopause; menstrual disorder; stress; autoimmune disease; prolactinoma; sterility; impotence; amenorrhea; lactorrhea; hyperpituitarism; Sheehan's syndrome Chairi-Frommel syndrome; Argonz-del Castilo syndrome; lyphoma; Forbes-Albright syndrome; spermatogenesis disorder.
                                                                                                                  61 ELKDWGPKNVIKMSTPAVNKMPHSFANLPLRFGRNVQEERSAGATANLPLRSGRNMEVSL 120
                                                                                                                                                                                                      ELKDWGPKNVIKMSTPAVNKMPHSFANLPLRFGRNVQEERSAGATANLPLRSGRNMEVSL 120
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prolactin
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2000JP-0378001.
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Matches 180; Conservative
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N-PSDB; AAH78475.
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The present sequence represents a bovine polypeptide which is a prolactin secretion regulating agent. The prolactin secretion regulating agent polypeptide and polynucleotide are used for the treatment and prevention of hypovarianism, sperm under development, osteoporosis, menopause, pituitary tumour, disnecephalon tumour, menstrual disorders, stress, pituitary tumour, disnecephalon tumour, menstrual disorders, stress, autoimmune disease, prolactinoma, sterility, impotence, amenorrhea, lactorrhea, hyperpliuitarism, Chairi-Frommel syndrome, Argonz-del Castilo syndrome, Forbes Albright syndrome, Ipphoma, Sheehan's syndrome
                                                                                                                                                                                                                                                                                    Bovine; prolactin secretion; hypocvarianism; sperm development; osteoporosis; lactation disorder; hypothyroidism; kidney failure; menopause; hyperprolactinemia; pituitary tumour; diencephalon tumour; menostrual disorder; stress; autoimmune disease; prolactinoma; sterility; impotence; amenorrhea; lactorrhea; hyperpituitarism; Sheehan's syndrome Chairi-Frommel syndrome; Argonz-del Castilo syndrome; lyphoma; Forbes-Albright syndrome; spermatogenesis disorder.
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                                         60 TFEEVKDWAPK--IKMNKPVVNKMPPSAANLPLRFGRNMEEERSTRAMAHLPLRLGKNRE 117
                           118 VSLVRRVPNLPQRFGRTTTAKSVCRMLSDLCQGSMHSPCANDLFYSMTCQHQEIQNPDQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New polypeptide, useful as a vasotropic, tranquilizing, immunosuppressive and gynecological agent comprises the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Habata Y,
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                                                                                                                                                                              AAG67749 standard; Protein; 196 AA
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                                                                                                 178 NLRRGFQKIDDAELKQEK 196
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                                                                                   QSRRLLFKKIDDAELKQEK 196
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      G protein coupled receptor protein and antibodies to it for treatment and diagnosis of nerve dispage.
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                                                                                                                                 121 VRRVPNLPQRFGRTTTARSVCRMLSDLCQGSWHSPCANDLFYSWTCQHQEIQNPDQRQSR 180
                                                               ELKDWGPKNVIKMSTPAVNKMPHSFANLPLRFGRNVQEERSAGATANLPLRSGRNMEVSL 120
                       Fukusumi
                                                                                                                                                                                                                                                                                                                           receptor; human; bovine; nervous system disorder;
        MEIISSKLFILLTLATSSLLTSNIFCADELVMSNLHSKENYDKYSEPRGYPKGERSLNFE
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; Pred. No. 2.4e-67;
13; Mismatches 37; Indels
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Kitada C;
                                                                                                                                                                                                                                                                                                                                            rat; mouse; somatostatin excretion
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                                                                                                                                                                                                                AAY93142 standard; Protein; 196
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71.9%;
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99JP-0060030.
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99JP-0221640.
99JP-0259818.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 71.9
Matches 143; Conservative
                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kikuchi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hosoya M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-387747/33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             196 AA;
                                                                                                                                                                                                                                                                                                                              G-protein coupled
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAA70502
                                                                                                                                                                                                                                                                                                                                                                                                 WO200029441-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                           25-MAY-2000
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                                                                                                                                                                                                                                                                                                                                                                       Bos taurus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seguence
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                                                                                                                                                                                                                                            AAY93142;
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Length 196;

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Yoshida H;

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FOELKDWGAKKDIKMSPAPANKVPHSAANLPLRFGRNIEDRRSPRARA-----NMEA 112
                                       SLVRRVPNLPQRFGRTTTAKSVCRMLSDLCQGSMHSPCANDLFYSMTCQHQEIQNPDQKQ
and spermatogenesis disorders
                                                                                                                                                                                                                                                                                                                                                                                                            (TAKE ) TAKEDA CHEM IND LTD.
                                                                                                                                                                                                                                                                                                                                                              06-MAR-2001; 2001WO-JP01716.
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|172 PRKRVFTETDDAERKQEK 189
                                                                                                                                                                                                                                                                                                                                                                                          2000JP-0378001
                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                 Watanabe T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               115; Conservative
                                                                    SRRLLFKKIDDAELKQEK
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N-PSDB; AAH78515.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       203 AA;
                                                                                                                                                                                                                                                                                                                      WO200166134-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Matsumoto Y,
                                                                                                                                                                                                                                                                                                                                                                                          07-DEC-2000;
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                                                                                                                                                                                                   Amino acid
                                                                                                                                                                                                                                                                                                     sp.
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                                                                                                                                                             AAG67756;
                                                                                                                                                                                                                                                                                                    Rattus
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           61
                                                                                                                       RESULT 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to the isolation of novel G-protein coupled receptor (GPCR) genes and their encoded proteins. This sequence represents the protein sequence of a rat GPCR. The DNAs and proteins are used for the treatment, prevention and diagnosis of disorders of the nervous system. The proteins and its fragments are also promoters
                                                            NFEELKDWGPKNVIKMSTPAVNKMPHSFANLPLRFGRNVQEERSAGATANLPLRSGRNME 117
                      60 TFEEVKDWAPK--IKMNKPVVNKMPPSAANLPLRFGRNMEEERSTRAMAHLPLRLGKNRE 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VSLVRRVPNLPQRFGRTTTAKSVCRMLSDLCQGSMHSPCANDLFYSMTCQHQEIQNPDQK 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MEIISSKLFILLTLATSSLLTSNIFCADELVMSNLHSKENYDKYSEPRGYPKG--ERSLN 58
                                                                                                                                                                                                                                                                                                                                                                                                                                            Fukusumi
                                                                                                                                                                                                                                          nervous system disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 21; Length 203;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     to it for
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Hinuma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    G protein coupled receptor protein and antibodies and diagnosis of nerve diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 46;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Shintani Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 1.2e-53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26; Mismatches
                                                                                                                                                                                                                                          G-protein coupled receptor; human; bovine; rat; mouse; somatostatin excretion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             54.3%; Score 552.5;
                                                                                                                                                                                                                        Novel rat G-protein coupled receptor #2.
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                                                                                                                                                              AAY93145 standard; Protein; 203 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                           K, Terao
Kitada C;
                                                                                          QSRRLLFKKIDDAELKQEK 196
                                                                                                     (TAKE ) TAKEDA CHEM IND LID.
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99JP-0106812
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       somatostatin excretion.
                                                                                                                                                                                                     (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Kikuchi
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hosoya M,
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Matches 115; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           203 AA;
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                                                                                                                                                                                 AAY93145;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 2;
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             28
                                                                                          178
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The present sequence represents a rat polypeptide which is a prolactin secretion regulating agent. The prolactin secretion regulating agent oblypeptide and polynucleotide are used for the treatment and prevention of hypocvarianism, sperm under development, osteoporosis, menopause, lactation disorders, hypothyroidism, kidney failure, hyperprolactinemia, pituitary tumour, diencephalon tumour, menstrual disorders, stress, autoimmune disease, prolactinoma, sterility, impotence, amenoriba, lactorinea, hyperpituitarism. Chairi-Frommel syndrome, Argonz-del Castilo syndrome, Forbes-Albright syndrome, lyphoma, Sheehan's syndrome
                                                                                                                                                                                                                                                                                                                                 Rat; prolactin secretion; hypoovarianism; sperm development; osteoporosis; lactation disorder; hypothyroidism; kidney failure; menopause; hypeprolactinemia; pituitary tumour; diencephalon tumour; menstrual disorder; stress; autoimmune disease; prolactinoma; sterility; impotence; amenorrhea; lactorrhea; hyperpituitarism; Sheehan's syndrome Chairi-Frommel syndrome; Argonz-del Castilo, syndrome;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New polypeptide, useful as a vasotropic, tranquilizing, immunosuppressive and gynecological agent comprises the prolactin secretion regulator -
                                                                                                                                                                                                                                               sequence of a rat prolactin secretion regulating agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yoshida H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Forbes-Albright syndrome; spermatogenesis disorder
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Habata Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     54.3%; Score 552.5; DB 2; 58.1%; Pred. No. 1.2e-53;
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AAG67756 standard; Protein; 203 AA.
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59 FEELKDWGPKNVIKMSTPAVNKMPHSFANLPLRFGRNVQEERSAGATANLPLRSGRNMEV 118

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59 FEELKDWGPKNVIKMSTPAVNKMPHSFANLPLRFGRNVQEERSAGATANLPLRSGRNMEV 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       secretion regulator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             203 AA;
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                                                                                                                                                                                                                                                                                                                                                           06-MAR-2000;
07-DEC-2000;
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                                                                                                                      RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to the isolation of novel G-protein coupled receptor (GPCR) genes and their encoded proteins. This sequence represents the protein sequence of a rat GPCR. The DNAs and proteins are used for the treatment, prevention and diagnosis of disorders of the nervous system. The proteins and its fragments are also promoters of somatostatin excretion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein coupled receptor protein and antibodies to it for treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MEIISSKLFILLTLATSSLLTSNIFCADELVMSNLHSKENYDKYSEPRGYPKG--ERSLN 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEELKDWGPKNVIKMSTPAVNKMPHSFANLPLRFGRNVQEERSAGATANLPLRSGRNMEV 118
                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                     Fukusumi
                                                                                                                                                                                                                                    human; bovine; nervous system disorder;
     1 MEIISSKRFILLTLATSSFLTSWTLCSDELMMPHFHSKEGYGKYYQLRGIPKGVKERSVT
                                                          119 SLVRRVPNLPQRFGRTTTAKSVCRMLSDLCQGSMHSPCANDLFYSMTCQHQEIQNPDQKQ
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57.6%; Pred. No. 5.7e-53;
11ve 26; Mismatches 47;
                                                                                                                                                                                                                                                                                                                                                                                                                     Shintani Y,
                                                                                                                                                                                                                  Novel rat G-protein coupled receptor #1
                                                                                                                                                             AAY93143 standard; Protein; 203 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                     K, Terao Y,
Kitada C;
                                                                                                                                                                                                                                              rat; mouse; somatostatin excretion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and diagnosis of nerve diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 2; Fig 5; 184pp; Japanese.
                                                                                                                                                                                                                                                                                                                                             99JP-0060030.
99JP-0106812.
99JP-0166672.
                                                                                                                                                                                                                                     receptor;
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|172 PRKRVFTETDDAERKQEK 189
                                                                                               179 SRRLLFKKIDDAELKQEK 196
                                                                                                                                                                                                (first entry)
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                                                                                                                                                                                                                                    G-protein coupled
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04-AUG-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                               AAY93143;
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The present sequence represents a rat polypeptide which is a prolactin secretion regulating agent. The prolactin secretion regulating agent polypeptide and polynucleotide are used for the treatment and prevention of hypocovarianism, sperm under development, osteoporosis, menopause, lactation disorders, hypothyroidism, kidney failure, hyperprolactinemia, pituitary tumour, diencephalon tumour, menstrual disorders, stress, autoimmune disease, prolactinoma, sterility, impotence, amenorrhea, lactorrhea, hyperpituitarism, Chairi-Frommel syndrome, Argonz-del Castilo syndrome, Forbes-Albright syndrome, lyphoma, Sheehan's syndrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bovine: prolactin secretion; hypoovarianism; sperm development; osteoporosis; lactation disorder; hypothyroidism; kidney failure; menopause; hyperprolactinemia; pituitary tumour; diencephalon tumour; menstrual disorder; stress; autoinmune disease; prolactinoma; sterility; impotence; amenorrhea; lactorrhea; hyperpituitarism; Sheehan's syndrome Chairi-Frommel syndrome; Argonz-del Castilo syndrome;
                                                                                 119 SLVRRVPNLPQRFGRTTTAKSVCRMLSDLCQGSMHSPCANDLFYSMTCQHQEIQNPDQKQ 178
                                                                                                                  1 MEIISSKLFILLTLATSSLLTSNIFCADELVMSNLHSKENYDKYSEPRGYPKG--ERSLN 58
Amino acid sequence of a rat prolactin secretion regulating agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     prolactin
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57.6%; Pred. No. 5.7e-53;
ive 26; Mismatches 47; 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                           AAG67750 standard; Protein; 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and spermatogenesis disorders.
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2000JP-0378001.
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                                                                                                                                                                                                                                                    SRRLLFKKIDDAELKQEK 196
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Best Local Similarity 57.6
Matches 114; Conservative
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113 GTRSHFPSLPQRFGR-TTARSP-KTPADLPQKPLHSLGSSELLYVMICQHQEIQSPGGKR 170
          FEELKDWGPKNVIKMSTPAVNKMPHSFANLPLRFGRNVQEERSAGATANLPLRSGRNMEV 118
                                                            SLVRRVPNLPQRFGRTTTAKSVCRMLSDLCQGSMHSPCANDLFYSMTCQHQEIQNPDQKQ
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171 TRGAFVETDDAERKPEK 188
                                                                                                               SRRLLFKKIDDAELKQEK 196
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                                                   for treatment
                                                                                      119 SLVRRVPNLPQRFGRTTTAKSVCRMLSDLCQGSMHSPCANDLFYSMTCQHQEIQNPDQKQ 178
                                                                                                    FEELKDWGPKNVIKMSTPAVNKMPHSFANLPLRFGRNVQEERSAGATANLPLRSGRNMEV 118
          MEIISSKRFILLTLATSSFLTSNTLCSDELMMPHFHSKEGYGKYYQLRGIPKGVKERSVT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fukusumi
                                                                                                                                                                                                                                                                                                                                  receptor; human; bovine; nervous system disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to the isolation of novel G-protein coupled
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 188;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hinuma
50.8%; Score 517; DB 21;
57.1%; Pred. No. 1e-49;
ive 22; Mismatches 51;
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                                                                                                                                                                                                                                                                                                          Novel mouse G-protein coupled receptor #1.
                                                                                                                                                                                                                               AAY93144 standard; Protein; 188 AA.
                                                                                                                                                                                                                                                                                                                                              mouse; somatostatin excretion
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soya M, Kitada C;
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172 PRKRVFTETDDAERKQEK 189
                                                                                                                                         SRRLLFKKIDDAELKQEK 196
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Matches 113; Conservative
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14-APR-1999,
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                                     59
                                                                                                               113
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                                                                                                                      osteoporosis; lactation disorder; hypothyroidism; kidney failure; menopause; hyperprolactinemia; pituitary tumour; diencephalon tumour; menstrual disorder; stress; autoimmune disease; prolactinoma; sterility; impotence; amenorrhea; lactorrhea; hyperpituitarism; Sheehan's syndrome Chairi-Frommel syndrome; Argonz-del Castilo syndrome; lyphoma; porbes-Albright syndrome; spermatogenesis disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      autoimmune disease, prolactinoma, sterility, impotence, amenorrhea, lactorrhea, hyperpituitarism, Chairi-Frommel syndrome, Argonz-del Castilo syndrome, Forbes-Albright syndrome, lyphoma, Sheehan's syndrome
                                                                                              Amino acid sequence of a murine prolactin secretion regulating agent.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               50.8%; Score 517; DB 22;
57.1%; Pred. No. 1e-49;
Mismatches 51;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 2; Page 156-157; 180pp; Japanese.
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AAG67751 standard; Protein; 188 AA
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                                                                                                                                                                                                                                                                                                                                                                                                     06-MAR-2000; 2000JP-0065752. 07-DEC-2000; 2000JP-0378001.
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                                                                  (first entry)
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Matches 113; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         secretion regulator
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                                                                10-DEC-2001
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                                 AAG67751;
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990S-0145276.
990S-0145913.
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990S-0146386.
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99US-0145087.
99US-0145089.
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99US-0145086.
99US-0145088.
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99US-0145145.
99US-0145218.
99US-0145224.
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990S-0139763.
990S-0139817.
990S-0140353.
990S-0140695.
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990S-0138034
990S-0138847
990S-0138847
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99US-0140991.
99US-0141287.
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99US-0142055.
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99US-0142920.
99US-0142977.
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99US-0143624.
99US-0144005.
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99US-0144086.
99US-0144325.
99US-0144331.
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99US-0137528.
99US-0137502.
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99US-0147204
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99US-0139463
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99US-0136782
                                                  04-JUN-1999;
07-JUN-1999;
08-JUN-1999;
10-JUN-1999;
10-JUN-1999;
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04-AUG-1999;
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18-JUN-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter;
                                                                     59 FEELKDWGPKNVIKMSTPAVNKMPHSFANLPLRFGRNVQEERSAGATANLPLRSGRNMEV 118 | 1:1|111 | 1|1|1|1 | 1:1| | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1 | 1|1|1
                                                                                                                                                                13 GTRSHFPSLPQRFGR-TTARSP-KTPADLPQKPLHSLGSSELYVMICQHQEIQSPGGKR 170
                                                                                                                                            SLVRRVPNLPQRFGRTTTAKSVCRMLSDLCQGSMHSPCANDLFYSMTCQHQEIQNPDQKQ 178
Arabidopsis thaliana protein fragment SEQ ID NO: 55810.
                                                                                                                                                                                                                                                                                                                                              AAG44544 standard; Protein; 354 AA
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99US-0134218.
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99US-0123180.
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99US-0128234.
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99US-0136392.
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99US-0132407
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99US-0129845
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99US-0130449
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99US-0131449
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